



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Suzuki, Shintaro
- (ii) TITLE OF INVENTION: Protocadherin Materials and Methods
- (iii) NUMBER OF SEQUENCES: 115
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, & Borun
 - (B) STREET: 233 South Wacker, 6300 Sears Tower
 - (C) CITY: Chicago
 - (D) STATE: Illinois
 - (E) COUNTRY: USA
 - (F) ZIP: 60606
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: Patent In Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE: 18 JUN 1998
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLCAITONJ DATA:
 - (A) APPLICATION NUMBER: US 08/263,161
 - (B) FILING DATE: 27 JUN 1994
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Greta E. Noland
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 - (C) REFERENCE/DOCKET NUMBER: 27866/34703
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 - (C) TELEX: 25-3856

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AARSSNNTNG AYTRYGA

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(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TTRCTRTTTC GNGGNNN

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(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 131 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AAGGGAGTGG ACTTTGAGGA GCAGCCTGAG CTTAGTCTCA TCCTCACGGC TTTGGATGGA 60
GGGACTCCAT CCAGGTCTGG GACTGCATTG GTTCAAGTGG AAGTCATAGA TGCCAATGAC 120
AACGCACCGT A 131

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Lys Gly Val Asp Phe Glu Glu Gln Pro Glu Leu Ser Leu Ile Leu Thr
1 5 10 15
Ala Leu Asp Gly Gly Thr Pro Ser Arg Ser Gly Thr Ala Leu Val Gln
20 25 30
Val Glu Val Ile Asp Ala Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AAACGCATGG ATTCGAGGA GTCTTCCTCC TACCAGATCT ATGTGCAAGC TACTGACCGG 60
GGACCA GTAC CCATGGCGGG TCATTGCAAG GTGTTGGTGG ACATTATAGA TGTGAACGAC 120
AACGCACCTA A 131

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Lys Ala Met Asp Phe Glu Glu Ser Ser Ser Tyr Gln Ile Tyr Val Gln
1 5 10 15
Ala Thr Asp Arg Gly Pro Val Pro Met Ala Gly His Cys Lys Val Leu
20 25 30
Val Asp Ile Ile Asp Val Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAGCGACTGG ACTTTGAGAC CCTGCAGACC TTCGAGTTCA GCGTGGGTGC CACAGACCAT 60
GGCTCCCCCT CGCTCCGCAG TCAGGCTCTG GTGCGCGTGG TGGTGCTGGA CCACAATGAC 120
AATGCCCCCA A 131

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Lys Arg Leu Asp Phe Glu Thr Leu Gln Thr Phe Glu Phe Ser Val Gly
1 5 10 15
Ala Thr Asp His Gly Ser Pro Ser Leu Arg Ser Gln Ala Leu Val Arg
20 25 30
Val Val Val Leu Asp His Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AAGGGCCTGG ATTACGAGGC ACTGCACTCC TTCGAGTTCT ACGTGGGCGC TACAGATGGA 60
GGCTCACCCG CGCTCAGCAG CCAGACTCTG GTGCGGATGG TGGTGCTGGA TGACAACGAC 120
AACGCCCCCTA A 131

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Lys Gly Leu Asp Tyr Glu Ala Leu Gln Ser Phe Glu Phe Tyr Val Gly
1 5 10 15

Ala Thr Asp Gly Gly Ser Pro Ala Leu Ser Ser Gln Thr Leu Val Arg
20 25 30

Met Val Val Leu Asp Asp Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AAGGCGTTTG ATTTTGAGGA TCAGAGAGAG TTCCAGCTAA CCGCTCATAT AAACGACGGA 60
GGTACCCCGG TTTTGGCCAC CAACATCAGC GTGAACATAT TTGTTACTGA CCGCAATGAC 120
AACGCCCCGC A 131

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Lys Ala Phe Asp Phe Glu Asp Gln Arg Glu Phe Gln Leu Thr Ala His
1 5 10 15
Ile Asn Asp Gly Gly Thr Pro Val Leu Ala Thr Asn Ile Ser Val Asn
20 25 30
Ile Phe Val Thr Asp Arg Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

| | |
|---|-----|
| AAGGCGGTGG ATTACGAAAT CACCAAGTCC TATGAGATAG ATGTTCAAGC CCAAGATCTG | 60 |
| GGTCCCAATT CTATTCCTGC TCATTGCAAA ATTATAATTA AGGTCGTGGA TGTCAACGAC | 120 |
| AACGCTCCCA A | 131 |

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 43 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Ala | Val | Asp | Tyr | Glu | Ile | Thr | Lys | Ser | Tyr | Glu | Ile | Asp | Val | Gln |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Ala | Gln | Asp | Leu | Gly | Pro | Asn | Ser | Ile | Pro | Ala | His | Cys | Lys | Ile | Ile |
| | | 20 | | | | | | 25 | | | | | 30 | | |
| Ile | Lys | Val | Val | Asp | Val | Asn | Asp | Asn | Ala | Pro | | | | | |
| | | 35 | | | | | | 40 | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 135 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

| | |
|---|-----|
| TATGACCATG ATTACGAGAC AACCAAAGAA TATACACTGC GGATCCGGGC CCAGGATGGT | 60 |
| GGCCGGACTC CACTTTCCAA CGTCTCCGGT CTAGTAACCG TGCAGGTCCT AGACATCAAC | 120 |
| GACAAATGCC CCCC | 135 |

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 44 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Tyr Asp His Asp Tyr Glu Thr Thr Lys Glu Tyr Thr Leu Arg Ile Arg
 1 5 10 15
 Ala Gln Asp Gly Gly Arg Thr Pro Leu Ser Asn Val Ser Gly Leu Val
 20 25 30
 Thr Val Gln Val Leu Asp Ile Asn Asp Asn Ala Pro
 35 40

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 129 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GGGGGGTCTGA TTACGAGGAG AACGGCATGT TAGAGATCGA CGTGCAGGCC AGAGACCTAG 60
 GACCTAACCC AATTCCAGCC CATTGCAAGG TCACAGTCAA GTCATCGAC CGCAATGATA 120
 ACGCCCCCA 129

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Arg Gly Val Asp Tyr Glu Glu Asn Gly Met Leu Glu Ile Asp Val Gln
 1 5 10 15
 Ala Arg Asp Leu Gly Pro Asn Pro Ile Pro Ala His Cys Lys Val Thr
 20 25 30
 Val Lys Leu Ile Asp Arg Asn Asp Asn Ala Pro
 35 40

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 131 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```
AAGGGGTTGG ACTACGAAGA CACCAAACTC CATGAGATTT ACATCCAGGC CAAAGACAAA      60
GGTGCCAATC CGGAAGGAGC GCATTGCAAA GTACTGGTAG AGGTTGTGGA CGTTAACGAC      120
AATGCCCCCTC A                                     131
```

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```
Lys Gly Leu Asp Tyr Glu Asp Thr Lys Leu His Glu Ile Tyr Ile Gln
 1           5           10           15
Ala Lys Asp Lys Gly Ala Asn Pro Glu Gly Ala His Cys Lys Val Leu
 20          25          30
Val Glu Val Val Asp Val Asn Asp Asn Ala Pro
 35          40
```

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 131 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```
AAGGGTTTGG ACTTTGAGCA AGTAGATGTC TACAAAATCC GCGTTGACGC GACGGACAAA      60
GGACACCCCTC CGATGGCAGG CCATTGCACT GTTTTAGTGA GGGTATTGGA TGAAAACGAC      120
AATGCGCCTC T                                     131
```


(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Lys Gly Leu Asp Phe Glu Gln Val Asp Val Tyr Lys Ile Arg Val Asp
1 5 10 15
Ala Thr Asp Lys Gly His Pro Pro Met Ala Gly His Cys Thr Val Leu
20 25 30
Val Arg Val Leu Asp Glu Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 134 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

AAGGGTATAG ACTTCGAGCA GATCAAGGAC TTCAGCTTTC AAGTGGAAGC CCGGGACGCC 60
GGCAGTCCCC AGGCGCTGTC CGGCAACTGC ACTGTCAACA TCTTGATAGT GGATCAGAAC 120
GACAACGCCC CTA 134

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Lys Gly Ile Asp Phe Glu Gln Ile Lys Asp Phe Ser Phe Gln Val Glu
1 5 10 15

Ala Arg Asp Ala Gly Ser Pro Gln Ala Leu Ala Gly Asn Thr Thr Val
 20 25 30
 Asn Ile Leu Ile Val Asp Gln Asn Asp Asn Ala Pro
 35 40

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 134 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AAGCCGTTTCG ACTATGAGCA AACCGCCAAC ACGCTGGCAC AGATTGACGC CGTGCTGGAA 60
 AAACAGGGCA GCAATAAATC GAGCATTCTG GATGCCACCA TTTTCCTGGC CGATAAAAC 120
 GACAATGCGC CAGA 134

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 44 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Lys Pro Phe Asp Tyr Glu Gln Thr Ala Asn Thr Leu Ala Gln Ile Asp
 1 5 10 15
 Ala Val Leu Glu Lys Gln Gly Ser Asn Lys Ser Ser Ile Leu Asp Ala
 20 25 30
 Thr Ile Phe Leu Ala Asp Lys Asn Asp Asn Ala Pro
 35 40

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 131 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

| | |
|---|-----|
| AAGCGGCTGG ATTTCGAACA GTTCCAGCAG CACAAGCTGC TCGTAAGGGC TGTTGATGGA | 60 |
| GGAATGCCGC CACTGAGCAG CGATGTGGTC GTCAGTGTGG ATGTCACCGA CCTCAACGAT | 120 |
| AACGCGCCCT A | 131 |

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

| | |
|---|--|
| Lys Arg Leu Asp Phe Glu Gln Phe Gln Gln His Lys Leu Leu Val Arg | |
| 1 5 10 15 | |
| Ala Val Asp Gly Gly Met Pro Pro Leu Ser Ser Asp Val Val Val Thr | |
| 20 25 30 | |
| Val Asp Val Thr Asp Leu Asn Asp Asn Ala Pro | |
| 35 40 | |

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 131 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

| | |
|---|-----|
| AAGGGGATAG ACTTTGAGAG TGAGAATTAC TATGAATTTG ATGTGCGGGC TCGCGATGGG | 60 |
| GGTTCTCCAG CCATGGAGCA ACATTGCAGC CTTGAGTGG ATCTGCTGGA CGTAAATGAC | 120 |
| AACGCCCCAC T | 131 |

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Lys Gly Ile Asp Phe Glu Ser Glu Asn Tyr Tyr Glu Phe Asp Val Arg
 1 5 10 15
 Ala Arg Asp Gly Gly Ser Pro Ala Met Glu Gln His Cys Ser Leu Arg
 20 25 30
 Val Asp Leu Leu Asp Val Asn Asp Asn Ala Pro
 35 40

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 131 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

AAGGCATTGG ACTTTGAGGC CCGGCGACTG TATTCGCTGA CAGTTCAGGC CACGGACCGA 60
 GCGGTGCCCT CGCTCACC GG GCGTGCCGAA GCGCTTATCC AGCTGCTAGA TGTCAACGAC 120
 AACGCACCCA T 131

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Lys Ala Leu Asp Phe Glu Ala Arg Arg Leu Tyr Ser Leu Thr Val Gln
 1 5 10 15
 Ala Thr Asp Arg Gly Val Pro Ser Leu Thr Gly Arg Ala Glu Ala Leu
 20 25 30
 Ile Gln Leu Leu Asp Val Asn Asp Asn Ala Pro
 35 40

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 125 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

```
AAGCCAATTG ATTACGAGGC AACTCCATAC TATAACATGG AAATTGTAGC CACAGACAGC      60
GGAGGTCTTT CGGGAAAATG CACTGTGTCT ATACAGGTGG TGGATGTGAA CGACAACGCC      120
CCCAA                                             125
```

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

```
Lys Pro Ile Asp Tyr Glu Ala Thr Pro Tyr Tyr Asn Met Glu Ile Val
1           5           10           15
Ala Thr Asp Ser Gly Gly Leu Ser Gly Lys Cys Thr Val Ser Ile Gln
                20           25           30
Val Val Asp Val Asn Asp Asn Ala Pro
                35           40
```

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 446 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

```
AAGCGGGTAG ACTTCGAAAT GTGCAAAGA TTTTACCTTG TGGTGAAGC TAAAGACGGA      60
GGCACCCAG CCCTCAGCAC GGCAGCCACT GTCAGCATCG ACCTCACAGA TGTGAATGAT      120
```

| | |
|---|-----|
| AACCCTCCTC GGTTCAGCCA AGATGTCTAC AGTGCTGTCA TCAGTGAGGA TGCCTTAGAG | 180 |
| GGGGACTCTG TCATTCTGCT GATAGCAGAA GATGTGGATA GCAAGCCTAA TGGACAGATT | 240 |
| CGGTTTTCCA TCGTGGGTGG AGATAGGGAC AATGAATTTG CTGTGATCC AATCTTGGGA | 300 |
| CTTGTAAG TTAAGAAGAA ACTGGACCGG GAGCGGGTGT CAGGATACTC CCTGCTCATC | 360 |
| CAGGCAGTAG ATAGTGGCAT TCCTGCAATG TCCTCAACGA CAACTGTCAA CATTGATATT | 420 |
| TCTGATGTGA ACGACAACGC CCCCCT | 446 |

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 148 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Lys | Arg | Val | Asp | Phe | Glu | Met | Cys | Lys | Arg | Phe | Tyr | Leu | Val | Val | Glu | 1 | 5 | 10 | 15 |
| Ala | Lys | Asp | Gly | Gly | Thr | Pro | Ala | Leu | Ser | Thr | Ala | Ala | Thr | Val | Ser | 20 | 25 | 30 | |
| Ile | Asp | Leu | Thr | Asp | Val | Asn | Asp | Asn | Pro | Pro | Arg | Phe | Ser | Gln | Asp | 35 | 40 | 45 | |
| Val | Tyr | Asp | Ala | Val | Ile | Ser | Glu | Asp | Ala | Leu | Glu | Gly | Asp | Ser | Val | 50 | 55 | 60 | |
| Ile | Leu | Leu | Ile | Ala | Glu | Asp | Val | Asp | Ser | Lys | Pro | Asn | Gly | Gln | Ile | 65 | 70 | 75 | 80 |
| Arg | Phe | Ser | Ile | Val | Gly | Gly | Asp | Arg | Asp | Asn | Glu | Phe | Ala | Val | Asp | 85 | 90 | 95 | |
| Pro | Ile | Leu | Gly | Leu | Val | Lys | Val | Lys | Lys | Lys | Leu | Asp | Arg | Glu | Arg | 100 | 105 | 110 | |
| Val | Ser | Gly | Tyr | Ser | Leu | Leu | Ile | Gln | Ala | Val | Asp | Ser | Gly | Ile | Pro | 115 | 120 | 125 | |
| Ala | Met | Ser | Ser | Thr | Thr | Thr | Val | Asn | Ile | Asp | Ile | Ser | Asp | Val | Asn | 130 | 135 | 140 | |
| Asp | Asn | Ala | Pro | 145 | | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 440 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

```
AAGGGGGTTG ATTATGAGAC AAACCCACGG CTACGACTGG TGCTACAGGC AGAGAGTGGA      60
GGAGCCTTTG CTTTCTCGGT GCTGACCCTG ACCCTTCAAG ATGCCAATGA CAATGCTCCC      120
CGTTTCCTGC AGCCTCACTA CGTGGCTTTC CTGCCAGAGT CCCGACCCTT GGAAGGGCCC      180
CTGCTGCAGG TGGAAGCAGA CGACCTGGAT CAAGGCTCTG GAGGACAGAT CTCCTACAGT      240
CTGGCTGCAT CCCAGCCAGC ACGGGGCTTG TTCCATGTAG ACCCAGCCAC AGGCACTATC      300
ACTACCACAG CCATCCTGGA CCGGGAAATC TGGGCTGAAA CACGGCTGGT ACTGATGGCC      360
ACAGACAGAG GAAGCCCAGC ATTGGTGGGC TCAGCTACCC TGACAGTGAT GGTCATCGAT      420
ACCAACGACA ATGCTCCCCT                                     440
```

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 146 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

```
Lys Gly Val Asp Tyr Glu Thr Asn Pro Arg Leu Arg Leu Val Leu Gln
 1           5           10          15
Ala Glu Ser Gly Gly Ala Phe Ala Phe Ser Val Leu Thr Leu Thr Leu
 20          25          30
Gln Asp Ala Asn Asp Asn Ala Pro Arg Phe Leu Gln Pro His Tyr Val
 35          40          45
Ala Phe Leu Pro Glu Ser Arg Pro Leu Glu Gly Pro Leu Leu Gln Val
 50          55          60
Glu Ala Asn Asp Leu Asp Gln Gly Ser Gly Gly Gln Ile Ser Tyr Ser
 65          70          75          80
Leu Ala Ala Ser Gln Pro Ala Arg Gly Leu Phe His Val Asp Pro Ala
 85          90          95
```

Thr Gly Thr Ile Thr Thr Thr Ala Ile Leu Asp Arg Glu Ile Trp Ala
 100 105 110
 Glu Thr Arg Leu Val Leu Met Ala Thr Asp Arg Gly Ser Pro Ala Leu
 115 120 125
 Val Gly Ser Ala Thr Leu Thr Val Met Val Ile Asp Thr Asn Asp Asn
 130 135 140
 Ala Pro
 145

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 124 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AAGGTCTCGA TTATGAGGCA ACTCCATATT ATAACGTGGA AATTGTAGCC ACAGATGGTG 60
 GGGGCCTTTC AGGAAAATGC ACTGTGGCTA TAGAAGTGGT GGATGTGAAC GACGGCGCTC 120
 CAAT 124

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Lys Gly Leu Asp Tyr Glu Ala Thr Pro Tyr Tyr Asn Val Glu Ile Val
 1 5 10 15
 Ala Thr Asp Gly Gly Ala Phe Asp Glu Asn Cys Thr Val Ala Ile Glu
 20 25 30
 Val Val Asp Val Asn Asp Asn Ala Pro
 35 40

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Asp Xaa Asn Glu Xaa Pro Xaa Phe
1 5

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Asp Xaa Asp Glu Xaa Pro Xaa Phe
1 5

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Asp Xaa Asn Asp Asn Xaa Pro Xaa Phe
1 5

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 131 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

AAGCGGATGG ATTTTGAAGA CACCAAACTC CATGAGATTT ACATCCAGGC CAAAGACAAA 60
GGTGCCAATC CCGAAGGAGC GCATTGCAAA GTACTTGTAG AGGTTGTAGA CGTAAACGAC 120
AACGCCCCAG T 131

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Leu Arg Met Asp Phe Glu Asp Thr Lys Leu His Glu Ile Tyr Ile Gln
1 5 10 15
Ala Lys Asp Lys Gly Ala Asn Pro Glu Gly Ala His Cys Lys Val Leu
20 25 30
Val Glu Val Val Asp Val Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

AAGGCTTTGG ATTACGAGGA TCAGAGAGAG TTCCAATAA CAGCTCATAT AAACGACGGA 60
GGTACCCCAG TCTTAGCCAC CAACATCAGC GTGAACGTAT TTGTTACTGA CCGCAATGAT 120
AACGCCCCCT A 131

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Lys Ala Leu Asp Tyr Glu Asp Gln Arg Glu Phe Gln Leu Thr Ala His
1 5 10 15
Ile Asn Asp Gly Gly Thr Pro Val Leu Ala Thr Asn Ile Ser Val Asn
20 25 30
Val Phe Val Thr Asp Arg Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

AAGCGCTTGG ACTACGAGGA GAGTAACAAT TATGAAATTC ACGTGGATGC TACAGATAAA 60
GGATACCCAC CTATGGTTGC TCACTGCACC GTACTCGTGG GAATCTTGGA TGAAAATGAC 120
AACGCACCCA T 131

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Lys Arg Leu Asp Tyr Glu Glu Ser Asn Asn Tyr Glu Ile His Val Asp
1 5 10 15
Ala Thr Asp Lys Gly Tyr Pro Pro Met Val Ala His Cys Thr Val Leu
20 25 30
Val Gly Ile Leu Asp Glu Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 131 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

```
AAACCGGTGG ACTACGAGAA AGTCAAAGAC TATACCATCG AGATCGTGGC TGTGGATTCC      60
GGCAACCCTC CACTCTCTAG CACCAACTCC CTCAAGGTGC AGGTGGTAGA CGTCAACGAT      120
AACGCCCCCTC T                                     131
```

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

```
Lys Pro Val Asp Tyr Glu Lys Val Lys Asp Tyr Thr Ile Glu Ile Val
1           5           10           15
Ala Val Asp Ser Gly Asn Pro Pro Leu Ser Ser Thr Asn Ser Leu Lys
20           25           30
Val Gln Val Val Asp Val Asn Asp Asn Ala Pro
35           40
```

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 131 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

```
AAGCCTTTTG ATTTGAGGA CACCAAATC CATGAGATTT ACATCCAGGC CAAAGACAAG      60
GGCGCCAATC CCGAAGGAGC ACATTGCAAA GTGTTGGTGG AGGTTGTGGA TGTGAACGAC      120
```

AATGCCCCCTC A

131

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Pro | Phe | Asp | Phe | Glu | Asp | Thr | Lys | Leu | His | Glu | Ile | Tyr | Ile | Gln |
| 1 | | | | 5 | | | | 10 | | | | | 15 | | |
| Ala | Lys | Asp | Lys | Gly | Ala | Asn | Pro | Glu | Gly | Ala | His | Cys | Lys | Val | Leu |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Val | Glu | Val | Val | Asp | Val | Asn | Asp | Asn | Ala | Pro | | | | | |
| | | | 35 | | | | | 40 | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 122 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| AAAGGTGTCG | ATTACGAGGT | GAGTCCACGG | CTGCGACTGG | TGCTGCAGGC | AGAGAGTCGA | 60 |
| GGAGCCTTTG | CCTTCACTGT | GCTGACCCTG | ACCCTGCAAG | ATGCCAACGA | CAACGCCCCG | 120 |
| AG | | | | | | 122 |

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Gly | Val | Asp | Tyr | Glu | Val | Ser | Pro | Arg | Leu | Arg | Leu | Val | Leu | Gln |
| 1 | | | | 5 | | | | 10 | | | | | 15 | | |

Ala Glu Ser Arg Gly Ala Phe Ala Phe Thr Val Leu Thr Leu Thr Leu
 20 25 30

Gln Asp Ala Asn Asp Asn Ala Pro
 35 40

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 131 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

AAAGGGATTG ATTACGAGCA GTTGAGAGAC CTACAGCTGT GGGTGACAGC CAGCGACAGC 60
 GGGGACCCGC CTCTTAGCAG CAACGTGTCA CTGAGCCTGT TTGTGCTGGA CCAGAACGAC 120
 AACGCCCCCC T 131

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Lys Gly Ile Asp Tyr Glu Gln Leu Arg Asp Leu Gln Leu Trp Val Thr
 1 5 10 15

Ala Ser Asp Ser Gly Asp Pro Pro Leu Ser Ser Asn Val Ser Leu Ser
 20 25 30

Leu Phe Val Leu Asp Gln Asn Asp Asn Ala Pro
 35 40

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 125 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

| | |
|---|-----|
| AAGGCGGTCG ATTTTGAGCG CACATCCTCT TATCAACTCA TCATTCAGGC CACCAATATG | 60 |
| GCAGGAATGG CTTCCAATGC TACAGTCAAT ATTCAGATTG TTGATGAAAA CGACAACGCC | 120 |
| CCCCA | 125 |

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Ala | Val | Asp | Phe | Glu | Arg | Thr | Ser | Ser | Tyr | Gln | Leu | Ile | Ile | Gln |
| 1 | | | | | 5 | | | | 10 | | | | | 15 | |
| Ala | Thr | Asn | Met | Ala | Gly | Met | Ala | Ser | Asn | Ala | Thr | Val | Asn | Ile | Gln |
| | | 20 | | | | | | 25 | | | | | 30 | | |
| Ile | Val | Asp | Glu | Asn | Asp | Asn | Ala | Pro | | | | | | | |
| | | 35 | | | | | 40 | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 131 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

| | |
|---|-----|
| AAACGGCTAG ACTTTGAAAA GATACAAAAA TATGTTGTAT GGATAGAGGC CAGAGATGGT | 60 |
| GGTTTCCCTC CTTTCTCCTC TTACGAGAAA CTTGATATAA CAGTATTAGA TGTCAACGAT | 120 |
| AACGCGCCTA A | 131 |

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Lys Arg Leu Asp Phe Glu Lys Ile Gln Lys Tyr Val Val Trp Ile Glu
1 5 10 15
Ala Arg Asp Gly Gly Phe Pro Pro Phe Ser Ser Tyr Glu Lys Leu Asp
20 25 30
Ile Thr Val Leu Asp Val Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

AAGGGGATCG ATTATGAGAA GGTCAAAGAC TACACCATTG AGATTGTGGC TGTGGACTCT 60
GGCAACCCCC CACTCTCCAG CACTAACTCC CTCAAGGTGC AGGTGGTGGA CGTCAATGAC 120
AACGCACCGT G 131

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Lys Gly Ile Asp Tyr Glu Lys Val Lys Asp Tyr Thr Ile Glu Ile Val
1 5 10 15
Ala Val Asp Ser Gly Asn Pro Pro Leu Ser Ser Thr Asn Ser Leu Lys
20 25 30
Val Gln Val Val Asp Val Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 131 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

```
AAGGGACTCG ACTACGAGGA TCGGCGGGAA TTTGAATTAA CAGTCATAT CAGCGATGGG      60
GGCACCCCGG TCCTAGCCAC CAACATCAGC GTGAACATAT TTGTCACTGA TCGCAACGAT      120
AATGCCCCCG T                                     131
```

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

```
Lys Gly Leu Asp Tyr Glu Asp Arg Arg Glu Phe Glu Leu Thr Ala His
1           5           10           15
Ile Ser Asp Gly Gly Thr Pro Val Leu Ala Thr Asn Ile Ser Val Asn
20          25          30
Ile Phe Val Thr Asp Arg Asn Asp Asn Ala Pro
35          40
```

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 470 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

```
AAGGGTTTGG ACTACGAGAC CACACAGGCC TACCAGCTCA CGGTCAACGC CACAGATCAA      60
GACAACACCA GGCCTCTGTC CACCCTGGCC AACTTGGCCA TCATCATCAC AGATGTCCAG      120
```

| | |
|---|-----|
| GACATGGACC CCATCTTCAT CAACCTGCCT TACAGCACCA ACATCTACGA GCATTCTCCT | 180 |
| CCGGGCACGA CGGTGCGCAT CATCACCGCC ATAGACCAGG ATCAAGGACG TCCCCGGGGC | 240 |
| ATTGGCTACA CCATCGTTTC AGGGAATACC AACAGCATCT TTGCCCTGGA CTACATCAGC | 300 |
| GGAGTGCTGA CTTTGAATGG CCTGCTGGAC CGGGAGAACC CCCTGTACAG CCATGGCTTC | 360 |
| ATCCTGACTG TGAAGGGCAC GGAGCTGAAC GATGACCGCA CCCCATCTGA CGCTACAGTC | 420 |
| ACCACGACCT TCAATATCCT GGTATTGAC ATCAACGACA ACGCCCCACT | 470 |

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Lys | Gly | Leu | Asp | Tyr | Glu | Thr | Thr | Gln | Ala | Tyr | Gln | Leu | Thr | Val | Asn | 1 | 5 | 10 | 15 |
| Ala | Thr | Asp | Gln | Asp | Asn | Thr | Arg | Pro | Leu | Ser | Thr | Leu | Ala | Asn | Leu | 20 | 25 | 30 | |
| Ala | Ile | Ile | Ile | Thr | Asp | Val | Gln | Asp | Met | Asp | Pro | Ile | Phe | Ile | Asn | 35 | 40 | 45 | |
| Leu | Pro | Tyr | Ser | Thr | Asn | Ile | Tyr | Glu | His | Ser | Pro | Pro | Gly | Thr | Thr | 50 | 55 | 60 | |
| Val | Arg | Ile | Ile | Thr | Ala | Ile | Asp | Gln | Asp | Gln | Gly | Arg | Pro | Arg | Gly | 65 | 70 | 75 | 80 |
| Ile | Gly | Tyr | Thr | Ile | Val | Ser | Gly | Asn | Thr | Asn | Ser | Ile | Phe | Ala | Leu | 85 | 90 | 95 | |
| Asp | Tyr | Ile | Ser | Gly | Val | Leu | Thr | Leu | Asn | Gly | Leu | Leu | Asp | Arg | Glu | 100 | 105 | 110 | |
| Asn | Pro | Leu | Tyr | Ser | Gly | Gly | Phe | Ile | Leu | Thr | Val | Lys | Gly | Thr | Glu | 115 | 120 | 125 | |
| Leu | Asn | Asp | Asp | Arg | Thr | Pro | Ser | Asp | Ala | Thr | Val | Thr | Thr | Thr | Phe | 130 | 135 | 140 | |
| Asn | Ile | Leu | Val | Ile | Asp | Ile | Asn | Asp | Asn | Ala | Pro | | | | | 145 | 150 | 155 | |

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 131 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

```
AAGGGGGTCG ATTACGAGGT ACTACAGGCC TTTGAGTTCC ACGTGAGCGC CACAGACCGA      60
GGCTCACCGG GGCTCAGCAG CCAGGCTCTG GTGCGCGTGG TGGTGCTGGA CGACAATGAC      120
AACGCTCCCCG T                                     131
```

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

```
Lys Gly Val Asp Tyr Glu Val Leu Gln Ala Phe Glu Phe His Val Ser
 1             5             10             15
Ala Thr Asp Arg Gly Ser Pro Gly Leu Ser Ser Gln Ala Leu Val Arg
      20             25             30
Val Val Val Leu Asp Asp Asn Asp Asn Ala Pro
      35             40
```

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 131 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

```
AAGGGGCTGG ATTATGAGCA GTTCCAGACC CTACAACCTGG GAGTGACCGC TAGTGACAGT      60
GGAAACCCAC CATTAAGAAG CAATATTTCA CTGACCCTTT TCGTGCTGGA CCAGAATGAT      120
```

AACGCCCCAA A

131

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Lys Gly Leu Asp Tyr Glu Gln Phe Gln Thr Leu Gln Leu Gly Val Thr
1 5 10 15
Ala Ser Asp Ser Gly Asn Pro Pro Leu Arg Ser Asn Ile Ser Leu Thr
20 25 30
Leu Phe Val Leu Asp Gln Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

AAGCGGGTTG ATTACGAGGA TGTCCAGAAA TACTCGCTGA GCATTAAGGC CCAGGATGGG 60
CGGCCCCCGC TCATCAATTC TTCAGGGGTG GTGTCTGTGC AGGTGCTGGA TGTCAACGAC 120
AATGCCCCGG A 131

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Lys Arg Val Asp Tyr Glu Asp Val Gln Lys Tyr Ser Leu Ser Ile Lys
1 5 10 15

Ala Gln Asp Gly Arg Pro Pro Leu Ile Asn Ser Ser Gly Val Val Ser
20 25 30

Val Gln Val Leu Asp Val Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 125 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

| | |
|---|-----|
| AAACCGGTAG ACTTTGAGCT ACAGCAGTTC TATGAAGTAG CTGTGGTGGC TTGGAAGTCT | 60 |
| GAGGGATTTC ATGTCAAAAG GGTCAATAAA GTGCAACTTT TAGATGACAA CGACAATGCC | 120 |
| CCGAT | 125 |

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

| | |
|---|--|
| Lys Pro Val Asp Phe Glu Leu Gln Gln Phe Tyr Glu Val Ala Val Val | |
| 1 5 10 15 | |
| Ala Trp Asn Ser Glu Gly Phe His Val Lys Arg Val Ile Lys Val Gln | |
| 20 25 30 | |
| Leu Leu Asp Asp Asn Asp Asn Ala Pro | |
| 35 40 | |

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 125 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

| | |
|---|-----|
| AAGGGATTAG ATTTTGAAAC TTTGCCCAT TACACATTGA TAATACAAGG AACTAACATG | 60 |
| GCTGGTTTGT CCACTAATAC AACGGTTCTA GTTCACTTGC AGGATGAGAA TGATAACGCC | 120 |
| CCAAA | 125 |

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Gly | Leu | Asp | Phe | Glu | Thr | Leu | Pro | Ile | Tyr | Thr | Leu | Ile | Ile | Gln |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Gly | Thr | Asn | Met | Ala | Gly | Leu | Ser | Thr | Asn | Thr | Thr | Val | Leu | Val | His |
| | | 20 | | | | | 25 | | | | | | 30 | | |
| Leu | Gln | Asp | Glu | Asn | Asp | Asn | Ala | Pro | | | | | | | |
| | | 35 | | | | | 40 | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 134 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

| | |
|--|-----|
| AAGCGGGCGG ATTTTCGAGGC GATCCGGGAG TACAGTCTGA GGATCAAAGC GCAGGACGGG | 60 |
| GGGCGGCCTC CCCTCAGCAA CACCACGGGC ATGGTCACAG TGCAGGTCGT GGACGTCAAT | 120 |
| GACAACGCAC CCCT | 134 |

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 44 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Lys Arg Ala Asp Phe Glu Ala Ile Arg Glu Tyr Ser Leu Arg Ile Lys
 1 5 10 15
 Ala Gln Asp Gly Gly Arg Pro Pro Leu Ser Asn Thr Thr Gly Met Val
 20 25 30
 Thr Val Gln Val Val Asp Val Asn Asp Asn Ala Pro
 35 40

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 131 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

AAGCGGTTGG ATTACGAAAA GGCATCGGAA TATGAAATCT ATGTTCAAGC CGCTGACAAA 60
 GGCGCTGTCC CTATGGCTGG CCATTGCAAA GTGTTGCTGG AGATCGTGGA TGTCAACGAC 120
 AACGCCCCCT T 131

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Lys Arg Leu Asp Tyr Glu Lys Ala Ser Glu Tyr Glu Ile Tyr Val Gln
 1 5 10 15
 Ala Ala Asp Lys Gly Ala Val Pro Met Ala Gly His Cys Lys Val Leu
 20 25 30
 Leu Glu Ile Val Asp Val Asn Asp Asn Ala Pro
 35 40

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

```
AAGGGGATCG ATTATGAGGA TCAGGTCTCT TACACATTAG CAGTAACAGC ACATGACTAT      60
GGCATCCCTC AAAAATCAGA CACTACCTAT TTGGAAATCT TAGTAATTGA TGTTAACGAC      120
AACGCGCCCC A                                     131
```

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

```
Lys Gly Ile Asp Tyr Glu Asp Gln Val Ser Tyr Thr Leu Ala Val Thr
1           5           10           15
Ala His Asp Tyr Gly Ile Pro Gln Lys Ser Asp Thr Thr Tyr Leu Glu
                20           25           30
Ile Leu Val Ile Asp Val Asn Asp Asn Ala Pro
35           40
```

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

```
AAAGGGTTAG ATTTTCGAGGG CACTAAAGAT TCAGCGTTTA AAATAGTGGC AGCTGACACA      60
GGGAAGCCCA GCCTCAACCA GACAGCCCTG GTGAGAGTAG AGCTGGAGGA TGAGAACGAC      120
```


AACGCCCCAA T

131

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Lys Gly Leu Asp Phe Glu Gly Thr Lys Asp Ser Ala Phe Lys Ile Val
1 5 10 15
Ala Ala Asp Thr Gly Lys Pro Ser Leu Asn Gln Thr Ala Leu Val Arg
20 25 30
Val Glu Leu Glu Asp Glu Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 130 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

AAGGGTGTGG ATTTTGAAAG TGTGCGTAGC TACAGGCTGG TTATTCGTGC TCAAGATGGA 60
GGCAGCCCCT CCAGAAGTAA CACCACCCAG CTCTTGGTCA ACGTCATCGA TCGAATGACA 120
ATGCGCCGCT 130

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Lys Gly Val Asp Phe Glu Ser Val Arg Ser Tyr Arg Leu Val Ile Arg
1 5 10 15

Ala Gln Asp Gly Gly Ser Pro Ser Arg Ser Asn Thr Thr Gln Leu Leu
20 25 30

Val Asn Val Ile Asp Val Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

AAGGGTGTGG ACTTCGAGCT GACACATCTG TATGAGATTT GGATTGAGGC TGCCGATGGA 60
GACACGCCAA GTCTGCGTAG TGTA ACTCTT ATAACGCTCA ACGTAACGGA TGCCAATGAC 120
AATGCTCCCA A 131

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Lys Gly Val Asp Phe Glu Leu Thr His Leu Tyr Glu Ile Trp Ile Glu
1 5 10 15
Ala Ala Asp Gly Asp Thr Pro Ser Leu Arg Ser Val Thr Leu Ile Thr
20 25 30
Leu Asn Val Thr Asp Ala Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 441 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

| | |
|---|-----|
| CAAGGCGTTT GATTTTGAAG AGACAAGTAG ATATGTGTTG AGTGTGGAAG CTAAGGATGG | 60 |
| AGGAGTACAC ACAGCTCACT GTAATGTTCA AATAGAAATT GTTGACGAGA ATGACAATGC | 120 |
| CCCAGAGGTG ACATTCATGT CCTTCTCTAA CCAGATTCCA GAGGATTCAG ACCTTGGAAC | 180 |
| TGTAATAGCC CTCATAAAAG TCGAGACAA GGATTCTGGG CAAAATGGCA TGGTGACATG | 240 |
| CTATACTCAG GAAGAAGTTC CTTTCAAATT AGAATCCACC TCGAAGAATT ATTACAAGCT | 300 |
| GGTGATTGCT GGAGCCCTAA ACCGGGAGCA GACAGCAGAC TACAACGTCA CAATCATAGC | 360 |
| CACCGACAAG GGCAAACCAG CCCTTTCCTC CAGGACAAGC ATCACCTGC ACATCTCCGA | 420 |
| CATCAACGAT AATGCCCCCG T | 441 |

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 146 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Lys | Ala | Phe | Asp | Phe | Glu | Glu | Thr | Ser | Arg | Tyr | Val | Leu | Ser | Val | Glu | 1 | 5 | 10 | 15 |
| Ala | Lys | Asp | Gly | Gly | Val | His | Thr | Ala | His | Cys | Asn | Val | Gln | Ile | Glu | 20 | 25 | 30 | |
| Ile | Val | Asp | Glu | Asn | Asp | Asn | Ala | Pro | Glu | Val | Thr | Phe | Met | Ser | Phe | 35 | 40 | 45 | |
| Ser | Asn | Gln | Ile | Pro | Glu | Asp | Ser | Asp | Leu | Gly | Thr | Val | Ile | Ala | Leu | 50 | 55 | 60 | |
| Ile | Lys | Val | Arg | Asp | Lys | Asp | Ser | Gly | Gln | Asn | Gly | Met | Val | Thr | Cys | 65 | 70 | 75 | 80 |
| Tyr | Thr | Gln | Glu | Glu | Val | Pro | Phe | Lys | Leu | Glu | Ser | Thr | Ser | Lys | Asn | 85 | 90 | 95 | |
| Tyr | Tyr | Lys | Leu | Val | Ile | Ala | Gly | Ala | Leu | Asn | Arg | Glu | Gln | Thr | Ala | 100 | 105 | 110 | |
| Asp | Tyr | Asn | Val | Thr | Ile | Ile | Ala | Thr | Asp | Lys | Gly | Lys | Pro | Ala | Leu | 115 | 120 | 125 | |
| Ser | Ser | Arg | Thr | Ser | Ile | Thr | Leu | His | Ile | Ser | Asp | Ile | Asn | Asp | Asn | 130 | 135 | 140 | |
| Ala | Pro | | | | | | | | | | | | | | | 145 | | | |

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 131 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

```
AAGCGAGTGG ATTACGAGGC CACTCGGAAT TATAAGCTGA GAGTTAAGGC TACTGATCTT      60
GGGATTCCAC CGAGATCTTC TAACATGACA CTGTTTCATTC ATGTCCTTGA TGTTAACGAC      120
AACGCTCCCT T                                                                131
```

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

```
Lys Arg Val Asp Tyr Glu Ala Thr Arg Asn Tyr Lys Leu Arg Val Lys
1           5           10
Ala Thr Asp Leu Gly Ile Pro Pro Arg Ser Ser Asn Met Thr Leu Phe
20          25          30
Ile His Val Leu Asp Val Asn Asp Asn Ala Pro
35          40
```

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4104 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 495..3572

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

| | |
|--|------|
| CCTCTATTTCG ACATTCTCTT TGGATTGTTT TGCTATAACT TGAAATTTGG GATGTCACAA | 60 |
| ACGAAACTGT CATCTGTTTC CGCCAAACTG TGGTTCTGCT AATCTCCCAG GCTGGCAGCA | 120 |
| TTGGAGACTT GCTGACTTCT TTCATCCCCC ACTCTTTTCA CCTGAAATTC CTTTCCTTGG | 180 |
| TTTGTCTCTA AGTCCTATGC TTCAGTCAGG GGCCAACCAA ATCTCACTGC CTCCTTTTTA | 240 |
| TCATGAAGCC TTTGATCACT GATAGTTCTT TTTATATCTT GAAAAATCAC CCTTCCCAGT | 300 |
| ACAGTTAATA TTTAGTATCT CTACTCATCT TGGCACTTAC TCACAGCTCC ATAATTCACT | 360 |
| CGTTTTTCGTA CCTCTTCATG GTGATGGGGA GCCCTTTGGA GGTGGTGACT GTGCTTTATA | 420 |
| CTCCTCATGA TGCTTCACAT GTGGCAGGCG TGGAGTGCCC GGAGGCGGCC CTCCTGATTC | 480 |
| TGGGGCCTCC CAGG ATG GAG CCC CTG AGG CAC AGC CCA GGC CCT GGG GGG | 530 |
| Met Glu Pro Leu Arg His Ser Pro Gly Pro Gly Gly | |
| 1 5 10 | |
| CAA CGG CTA CTG CTG CCC TCC ATG CTG CTA GCA CTG CTG CTC CTG CTG | 578 |
| Gln Arg Leu Leu Pro Ser Met Leu Leu Ala Leu Leu Leu Leu Leu | |
| 15 20 25 | |
| GCT CCA TCC CCA GGC CAC GCC ACT CGG GTA GTG TAC AAG GTG CCG GAG | 626 |
| Ala Pro Ser Pro Gly His Ala Thr Arg Val Val Tyr Lys Val Pro Glu | |
| 30 35 40 | |
| GAA CAG CCA CCC AAC ACC CTC ATT GGG AGC CTC GCA GCC GAC TAT GGT | 674 |
| Glu Gln Pro Pro Asn Thr Leu Ile Gly Ser Leu Ala Ala Asp Tyr Gly | |
| 45 50 55 60 | |
| TTT CCA GAT GTG GGG CAC CTG TAC AAG CTA GAG GTG GGT GCC CCG TAC | 722 |
| Phe Pro Asp Val Gly His Leu Tyr Lys Leu Glu Val Gly Ala Pro Tyr | |
| 65 70 75 | |
| CTT CGC GTG GAT GGC AAG ACA GGT GAC ATT TTC ACC ACC GAG ACC TCC | 770 |
| Leu Arg Val Asp Gly Lys Thr Gly Asp Ile Phe Thr Thr Glu Thr Ser | |
| 80 85 90 | |
| ATC GAC CGT GAG GGG CTC CGT GAA TGC CAG AAC CAG CTC CCT GGT GAT | 818 |
| Ile Asp Arg Glu Gly Leu Arg Glu Cys Gln Asn Gln Leu Pro Gly Asp | |
| 95 100 105 | |
| CCC TGC ATC CTG GAG TTT GAG GTA TCT ATC ACA GAC CTC GTG CAG AAT | 866 |
| Pro Cys Ile Leu Glu Phe Glu Val Ser Ile Thr Asp Leu Val Gln Asn | |
| 110 115 120 | |
| GCG AGC CCC CGG CTG CTA GAG GGC CAG ATA GAA GTA CAA GAC ATC AAT | 914 |
| Ala Ser Pro Arg Leu Leu Glu Gly Gln Ile Glu Val Gln Asp Ile Asn | |
| 125 130 135 140 | |
| GAC AAC ACA CCC AAC TTC GCC TCA CCA GTC ATC ACT CTG GCC ATC CCT | 962 |
| Asp Asn Thr Pro Asn Phe Ala Ser Pro Val Ile Thr Leu Ala Ile Pro | |
| 145 150 155 | |
| GAG AAC ACC AAC ATC GGC TCA CTC TTC CCC ATC CCG CTG GCT TCA GAC | 1010 |
| Glu Asn Thr Asn Ile Gly Ser Leu Phe Pro Ile Pro Leu Ala Ser Asp | |
| 160 165 170 | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| CGT | GAT | GCT | GGT | CCC | AAC | GGT | GTG | GCA | TCC | TAT | GAG | CTG | CAG | GTG | GCA | 1058 |
| Arg | Asp | Ala | Gly | Pro | Asn | Gly | Val | Ala | Ser | Tyr | Glu | Leu | Gln | Val | Ala | |
| | 175 | | | | | | 180 | | | | | 185 | | | | |
| GAG | GAC | CAG | GAG | GAG | AAG | CAA | CCA | CAG | CTC | ATT | GTG | ATG | GGC | AAC | CTG | 1106 |
| Glu | Asp | Gln | Glu | Glu | Lys | Gln | Pro | Gln | Leu | Ile | Val | Met | Gly | Asn | Leu | |
| | 190 | | | | | 195 | | | | | 200 | | | | | |
| GAC | CGT | GAG | CGC | TGG | GAC | TCC | TAT | GAC | CTC | ACC | ATC | AAG | GTG | CAG | GAT | 1154 |
| Asp | Arg | Glu | Arg | Trp | Asp | Ser | Tyr | Asp | Leu | Thr | Ile | Lys | Val | Gln | Asp | |
| 205 | | | | | 210 | | | | | 215 | | | | | 220 | |
| GGC | GGC | AGC | CCC | CCA | CGC | GCC | ACG | AGT | GCC | CTG | CTG | CGT | GTC | ACC | GTG | 1202 |
| Gly | Gly | Ser | Pro | Pro | Arg | Ala | Thr | Ser | Ala | Leu | Leu | Arg | Val | Thr | Val | |
| | | | | 225 | | | | | 230 | | | | | 235 | | |
| CTT | GAC | ACC | AAT | GAC | AAC | GCC | CCC | AAG | TTT | GAG | CGG | CCC | TCC | TAT | GAG | 1250 |
| Leu | Asp | Thr | Asn | Asp | Asn | Ala | Pro | Lys | Phe | Glu | Arg | Pro | Ser | Tyr | Glu | |
| | | | 240 | | | | | 245 | | | | | 250 | | | |
| GCC | GAA | CTA | TCT | GAG | AAT | AGC | CCC | ATA | GGC | CAC | TCG | GTC | ATC | CAG | GTG | 1298 |
| Ala | Glu | Leu | Ser | Glu | Asn | Ser | Pro | Ile | Gly | His | Ser | Val | Ile | Gln | Val | |
| | 255 | | | | | | 260 | | | | | 265 | | | | |
| AAG | GCC | AAT | GAC | TCA | GAC | CAA | GGT | GCC | AAT | GCA | GAA | ATC | GAA | TAC | ACA | 1346 |
| Lys | Ala | Asn | Asp | Ser | Asp | Gln | Gly | Ala | Asn | Ala | Glu | Ile | Glu | Tyr | Thr | |
| | 270 | | | | | 275 | | | | | 280 | | | | | |
| TTC | CAC | CAG | GCG | CCC | GAA | GTT | GTG | AGG | CGT | CTT | CTT | CGA | CTG | GAC | AGG | 1394 |
| Phe | His | Gln | Ala | Pro | Glu | Val | Val | Arg | Arg | Leu | Leu | Arg | Leu | Asp | Arg | |
| 285 | | | | | 290 | | | | | 295 | | | | | 300 | |
| AAC | ACT | GGA | CTT | ATC | ACT | GTT | CAG | GGC | CCG | GTG | GAC | CGT | GAG | GAC | CTA | 1442 |
| Asn | Thr | Gly | Leu | Ile | Thr | Val | Gln | Gly | Pro | Val | Asp | Arg | Glu | Asp | Leu | |
| | | | | 305 | | | | | 310 | | | | | 315 | | |
| AGC | ACC | CTG | CGC | TTC | TCA | GTG | CTT | GCT | AAG | GAC | CGA | GGC | ACC | AAC | CCC | 1490 |
| Ser | Thr | Leu | Arg | Phe | Ser | Val | Leu | Ala | Lys | Asp | Arg | Gly | Thr | Asn | Pro | |
| | | | 320 | | | | | 325 | | | | | 330 | | | |
| AAG | AGT | GCC | CGT | GCC | CAG | GTG | GTT | GTG | ACC | GTG | AAG | GAC | ATG | AAT | GAC | 1538 |
| Lys | Ser | Ala | Arg | Ala | Gln | Val | Val | Val | Thr | Val | Lys | Asp | Met | Asn | Asp | |
| | | 335 | | | | 340 | | | | | | 345 | | | | |
| AAT | GCC | CCC | ACC | ATT | GAG | ATC | CGG | GGC | ATA | GGG | CTA | GTG | ACT | CAT | CAA | 1586 |
| Asn | Ala | Pro | Thr | Ile | Glu | Ile | Arg | Gly | Ile | Gly | Leu | Val | Thr | His | Gln | |
| | 350 | | | | | 355 | | | | | 360 | | | | | |
| GAT | GGG | ATG | GCT | AAC | ATC | TCA | GAG | GAT | GTG | GCA | GAG | GAG | ACA | GCT | GTG | 1634 |
| Asp | Gly | Met | Ala | Asn | Ile | Ser | Glu | Asp | Val | Ala | Glu | Glu | Thr | Ala | Val | |
| 365 | | | | | 370 | | | | | 375 | | | | | 380 | |
| GCC | CTG | GTG | CAG | GTG | TCT | GAC | CGA | GAT | GAG | GGA | GAG | AAT | GCA | GCT | GTC | 1682 |
| Ala | Leu | Val | Gln | Val | Ser | Asp | Arg | Asp | Glu | Gly | Glu | Asn | Ala | Ala | Val | |
| | | | | 385 | | | | | 390 | | | | | 395 | | |
| ACC | TGT | GTG | GTG | GCA | GGT | GAT | GTG | CCC | TTC | CAG | CTG | CGC | CAG | GCC | AGT | 1730 |
| Thr | Cys | Val | Val | Ala | Gly | Asp | Val | Pro | Phe | Gln | Leu | Arg | Gln | Ala | Ser | |
| | | | 400 | | | | | 405 | | | | | | 410 | | |

| | | | | | | | | | | | | | | | | |
|-------------------|-------------------|-------------------|-------------------|------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| GAG Glu | ACA Thr | GGC Gly 415 | AGT Ser | GAC Asp | AGC Ser | AAG Lys | AAG Lys 420 | AAG Lys | TAT Tyr | TTC Phe | CTG Leu | CAG Gln 425 | ACT Thr | ACC Thr | ACC Thr | 1778 |
| CCG Pro | CTA Leu 430 | GAC Asp | TAC Tyr | GAG Glu | AAG Lys | GTC Val 435 | AAA Lys | GAC Asp | TAC Tyr | ACC Thr | ATT Ile 440 | GAG Glu | ATT Ile | GTG Val | GCT Ala | 1826 |
| GTG Val 445 | GAC Asp | TCT Ser | GGC Gly | AAC Asn | CCC Pro 450 | CCA Pro | CTC Leu | TCC Ser | AGC Ser | ACT Thr 455 | AAC Asn | TCC Ser | CTC Leu | AAG Lys | GTG Val 460 | 1874 |
| CAG Gln | GTG Val | GTG Val | GAC Asp 465 | GTC Val | AAT Asn | GAC Asp | AAC Asn | GCA Ala | CCT Pro 470 | GTC Val | TTC Phe | ACT Thr | CAG Gln | AGT Ser 475 | GTC Val | 1922 |
| ACT Thr | GAG Glu | GTC Val 480 | GCC Ala | TTC Phe | CCG Pro | GAA Glu | AAC Asn 485 | AAC Asn | AAG Lys | CCT Pro | GGT Gly | GAA Glu 490 | GTG Val | ATT Ile | GCT Ala | 1970 |
| GAG Glu | ATC Ile | ACT Thr 495 | GCC Ala | AGT Ser | GAT Asp | GCT Ala | GAC Asp 500 | TCT Ser | GGC Gly | TCT Ser | AAT Asn 505 | GCT Ala | GAG Glu | CTG Leu | GTT Val | 2018 |
| TAC Tyr | TCT Ser 510 | CTG Leu | GAG Glu | CCT Pro | GAG Glu | CCG Pro 515 | GCT Ala | GCT Ala | AAG Lys | GGC Gly 520 | CTC Leu | TTC Phe | ACC Thr | ATC Ile | TCA Ser | 2066 |
| CCC Pro 525 | GAG Glu | ACT Thr | GGA Gly | GAG Glu | ATC Ile 530 | CAG Gln | GTG Val | AAG Lys | ACA Thr 535 | TCT Ser 535 | CTG Leu | GAT Asp | CGG Arg | GAA Glu | CAG Gln 540 | 2114 |
| CGG Arg | GAG Glu | AGC Ser | TAT Tyr 545 | GAG Glu | TTG Leu | AAG Lys | GTG Val | GTG Val | GCA Ala 550 | GCT Ala | GAC Asp | CGG Arg | GGC Gly | AGT Ser 555 | CCT Pro | 2162 |
| AGC Ser | CTC Leu | CAG Gln 560 | GGC Gly | ACA Thr | GCC Ala | ACT Thr | GTC Val 565 | CTT Leu | GTC Val | AAT Asn | GTG Val | CTG Leu | GAC Asp 570 | TGC Cys | AAT Asn | 2210 |
| GAC Asp | AAT Asn 575 | GAC Asp | CCC Pro | AAA Lys | TTT Phe | ATG Met | CTG Leu 580 | AGT Ser | GGC Gly | TAC Tyr | AAC Asn 585 | TTC Phe | TCA Ser | GTG Val | ATG Met | 2258 |
| GAG Glu | AAC Asn 590 | ATG Met | CCA Pro | GCA Ala | CTG Leu | AGT Ser 595 | CCA Pro | GTG Val | GGC Gly | ATG Met | GTG Val 600 | ACT Thr | GTC Val | ATT Ile | GAT Asp | 2306 |
| GGA Gly 605 | GAC Asp | AAG Lys | GGG Gly | GAG Glu | AAT Asn 610 | GCC Ala | CAG Gln | GTG Val | CAG Gln | CTC Leu 615 | TCA Ser | GTG Val | GAG Glu | CAG Gln | GAC Asp 620 | 2354 |
| AAC Asn | GGT Gly | GAC Asp | TTT Phe 625 | GTT Val | ATC Ile | CAG Gln | AAT Asn | GGC Gly | ACA Thr 630 | GGC Gly | ACC Thr | ATC Ile | CTA Leu | TCC Ser 635 | AGC Ser | 2402 |
| CTG Leu | AGC Ser | TTT Phe 640 | GAT Asp | CGA Arg | GAG Glu | CAA Gln | CAA Gln | AGC Ser 645 | ACC Thr | TAC Tyr | ACC Thr | TTC Phe | CAG Gln 650 | CTG Leu | AAG Lys | 2450 |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| GCA | GTG | GAT | GGT | GGC | GTC | CCA | CCT | CGC | TCA | GCT | TAC | GTT | GGT | GTC | ACC | 2498 |
| Ala | Val | Asp | Gly | Gly | Val | Pro | Pro | Arg | Ser | Ala | Tyr | Val | Gly | Val | Thr | |
| | | 655 | | | | | 660 | | | | | 665 | | | | |
| ATC | AAT | GTG | CTG | GAC | GAG | AAT | GAC | AAC | GCA | CCC | TAT | ATC | ACT | GCC | CCT | 2546 |
| Ile | Asn | Val | Leu | Asp | Glu | Asn | Asp | Asn | Ala | Pro | Tyr | Ile | Thr | Ala | Pro | |
| | | 670 | | | | | 675 | | | | 680 | | | | | |
| TCT | AAC | ACC | TCT | CAC | AAG | CTG | CTG | ACC | CCC | CAG | ACA | CGT | CTT | GGT | GAG | 2594 |
| Ser | Asn | Thr | Ser | His | Lys | Leu | Leu | Thr | Pro | Gln | Thr | Arg | Leu | Gly | Glu | |
| | | | | | 690 | | | | | 695 | | | | | 700 | |
| ACG | GTC | AGC | CAG | GTG | GCA | GCC | GAG | GAC | TTT | GAC | TCT | GGT | GTC | AAT | GCC | 2642 |
| Thr | Val | Ser | Gln | Val | Ala | Ala | Glu | Asp | Phe | Asp | Ser | Gly | Val | Asn | Ala | |
| | | | | 705 | | | | | 710 | | | | | | 715 | |
| GAG | CTG | ATC | TAC | AGC | ATT | GCA | GGT | GGC | AAC | CCT | TAT | GGA | CTC | TTC | CAG | 2690 |
| Glu | Leu | Ile | Tyr | Ser | Ile | Ala | Gly | Gly | Asn | Pro | Tyr | Gly | Leu | Phe | Gln | |
| | | | 720 | | | | | 725 | | | | | 730 | | | |
| ATT | GGG | TCA | CAT | TCA | GGT | GCC | ATC | ACC | CTG | GAG | AAG | GAG | ATT | GAG | CGG | 2738 |
| Ile | Gly | Ser | His | Ser | Gly | Ala | Ile | Thr | Leu | Glu | Lys | Glu | Ile | Glu | Arg | |
| | | | 735 | | | | 740 | | | | | 745 | | | | |
| CGC | CAC | CAT | GGG | CTA | CAC | CGC | CTG | GTG | GTG | AAG | GTC | AGT | GAC | CGC | GGC | 2786 |
| Arg | His | His | Gly | Leu | His | Arg | Leu | Val | Val | Lys | Val | Ser | Asp | Arg | Gly | |
| | | | 750 | | | 755 | | | | | 760 | | | | | |
| AAG | CCC | CCA | CGC | TAT | GGC | ACA | GCC | TTG | GTC | CAT | CTT | TAT | GTC | AAT | GAG | 2834 |
| Lys | Pro | Pro | Arg | Tyr | Gly | Thr | Ala | Leu | Val | His | Leu | Tyr | Val | Asn | Glu | |
| | | | | 770 | | | | | | 775 | | | | | 780 | |
| ACT | CTG | GCC | AAC | CGC | ACG | CTG | CTG | GAG | ACC | CTC | CTG | GGC | CAC | AGC | CTG | 2882 |
| Thr | Leu | Ala | Asn | Arg | Thr | Leu | Leu | Glu | Thr | Leu | Leu | Gly | His | Ser | Leu | |
| | | | | 785 | | | | | 790 | | | | | | 795 | |
| GAC | ACG | CCG | CTG | GAT | ATT | GAC | ATT | GCT | GGG | GAT | CCA | GAA | TAT | GAG | CGC | 2930 |
| Asp | Thr | Pro | Leu | Asp | Ile | Asp | Ile | Ala | Gly | Asp | Pro | Glu | Tyr | Glu | Arg | |
| | | | 800 | | | | | 805 | | | | | 810 | | | |
| TCC | AAG | CAG | CGT | GGC | AAC | ATT | CTC | TTT | GGT | GTG | GTG | GCT | GGT | GTG | GTG | 2978 |
| Ser | Lys | Gln | Arg | Gly | Asn | Ile | Leu | Phe | Gly | Val | Val | Ala | Gly | Val | Val | |
| | | 815 | | | | | 820 | | | | | 825 | | | | |
| GCC | GTG | GCC | TTG | CTC | ATC | GCC | CTG | GCG | GTT | CTT | GTG | CGC | TAC | TGC | AGA | 3026 |
| Ala | Val | Ala | Leu | Leu | Ile | Ala | Leu | Ala | Val | Leu | Val | Arg | Tyr | Cys | Arg | |
| | | 830 | | | | 835 | | | | | 840 | | | | | |
| CAG | CGG | GAG | GCC | AAA | AGT | GGT | TAC | CAG | GCT | GGT | AAG | AAG | GAG | ACC | AAG | 3074 |
| Gln | Arg | Glu | Ala | Lys | Ser | Gly | Tyr | Gln | Ala | Gly | Lys | Lys | Glu | Thr | Lys | |
| | | | | | 850 | | | | | 855 | | | | | 860 | |
| GAC | CTG | TAT | GCC | CCC | AAG | CCC | AGT | GGC | AAG | GCC | TCC | AAG | GGA | AAC | AAA | 3122 |
| Asp | Leu | Tyr | Ala | Pro | Lys | Pro | Ser | Gly | Lys | Ala | Ser | Lys | Gly | Asn | Lys | |
| | | | | 865 | | | | | 870 | | | | | 875 | | |
| AGC | AAA | GGC | AAG | AAG | AGC | AAG | TCC | CCA | AAG | CCC | GTG | AAG | CCA | GTG | GAG | 3170 |
| Ser | Lys | Gly | Lys | Lys | Ser | Lys | Ser | Pro | Lys | Pro | Val | Lys | Pro | Val | Glu | |
| | | | 880 | | | | | 885 | | | | | 890 | | | |

| | |
|---|------|
| GAC GAG GAT GAG GCC GGG CTG CAG AAG TCC CTC AAG TTC AAC CTG ATG Asp Glu Asp Glu Ala Gly Leu Gln Lys Ser Leu Lys Phe Asn Leu Met 895 900 905 | 3218 |
| AGC GAT GCC CCT GGG GAC AGT CCC CGC ATC CAC CTG CCC CTC AAC TAC Ser Asp Ala Pro Gly Asp Ser Pro Arg Ile His Leu Pro Leu Asn Tyr 910 915 920 | 3266 |
| CCA CCA GGC AGC CCT GAC CTG GGC CGC CAC TAT CGC TCT AAC TCC CCA Pro Pro Gly Ser Pro Asp Leu Gly Arg His Tyr Arg Ser Asn Ser Pro 925 930 935 940 | 3314 |
| CTG CCT TCC ATC CAG CTG CAG CCC CAG TCA CCC TCA GCC TCC AAG AAG Leu Pro Ser Ile Gln Leu Gln Pro Gln Ser Pro Ser Ala Ser Lys Lys 945 950 955 | 3362 |
| CAC CAG GTG GTA CAG GAC CTG CCA CCT GCA AAC ACA TTC GTG GGC ACC His Gln Val Val Gln Asp Leu Pro Pro Ala Asn Thr Phe Val Gly Thr 960 965 970 | 3410 |
| GGG GAC ACC ACG TCC ACG GGC TCT GAG CAG TAC TCC GAC TAC AGC TAC Gly Asp Thr Thr Ser Thr Gly Ser Glu Gln Tyr Ser Asp Tyr Ser Tyr 975 980 985 | 3458 |
| CGC ACC AAC CCC CCC AAA TAC CCC AGC AAG CAG GTA GGC CAG CCC TTT Arg Thr Asn Pro Pro Lys Tyr Pro Ser Lys Gln Val Gly Gln Pro Phe 990 995 1000 | 3506 |
| CAG CTC AGC ACA CCC CAG CCC CTA CCC CAC CCC TAC CAC GGA GCC ATC Gln Leu Ser Thr Pro Gln Pro Leu Pro His Pro Tyr His Gly Ala Ile 1005 1010 1015 1020 | 3554 |
| TGG ACC GAG GTG TGG GAG TGATGGAGCA GGTTTACTGT GCCTGCCCCGT Trp Thr Glu Val Trp Glu 1025 | 3602 |
| GTTGGGGGCC AGCCTGAGCC AGCAGTGGGA GGTGGGGCCT TAGTGCCTCA CCGGGCACAC | 3662 |
| GGATTAGGCT GAGTGAAGAT TAAGGGAGGG TGTGCTCTGT GGTCTCCTCC CTGCCCTCTC | 3722 |
| CCCACTGGGG AGAGACCTGT GATTTGCCAA GTCCCTGGAC CCTGGACCAG CTA CTGGGGCC | 3782 |
| TTATGGGTTG GGGGTGGTAG GCAGGTGAGC GTAAGTGGGG AGGGAAATGG GTAAGAAGTC | 3842 |
| TACTCCAAAC CTAGGTCTCT ATGTCAGACC AGACCTAGGT GCTTCTCTAG GAGGGAAACA | 3902 |
| GGGAGACCTG GGGTCCTGTG GATAACTGAG TGGGGAGTCT GCCAGGGGAG GGCACCTTCC | 3962 |
| CATTGTGCCT TCTGTGTGTA TTGTGCATTA ACCTCTTCCT CACCACTAGG CTTCTGGGGC | 4022 |
| TGGGTCCCAC ATGCCCTTGA CCCTGACAAT AAAGTTCTCT ATTTTGGAA AAAAAAAAAA | 4082 |
| AAAAAAAAAA AAAAAAAAAA AA | 4104 |

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1026 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

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Met Glu Pro Leu Arg His Ser Pro Gly Pro Gly Gly Gln Arg Leu Leu
 1              5              10              15

Leu Pro Ser Met Leu Leu Ala Leu Leu Leu Leu Ala Pro Ser Pro
      20              25              30

Gly His Ala Thr Arg Val Val Tyr Lys Val Pro Glu Glu Gln Pro Pro
      35              40              45

Asn Thr Leu Ile Gly Ser Leu Ala Ala Asp Tyr Gly Phe Pro Asp Val
      50              55              60

Gly His Leu Tyr Lys Leu Glu Val Gly Ala Pro Tyr Leu Arg Val Asp
      65              70              75              80

Gly Lys Thr Gly Asp Ile Phe Thr Thr Glu Thr Ser Ile Asp Arg Glu
      85              90              95

Gly Leu Arg Glu Cys Gln Asn Gln Leu Pro Gly Asp Pro Cys Ile Leu
      100              105              110

Glu Phe Glu Val Ser Ile Thr Asp Leu Val Gln Asn Ala Ser Pro Arg
      115              120              125

Leu Leu Glu Gly Gln Ile Glu Val Gln Asp Ile Asn Asp Asn Thr Pro
      130              135              140

Asn Phe Ala Ser Pro Val Ile Thr Leu Ala Ile Pro Glu Asn Thr Asn
      145              150              155              160

Ile Gly Ser Leu Phe Pro Ile Pro Leu Ala Ser Asp Arg Asp Ala Gly
      165              170              175

Pro Asn Gly Val Ala Ser Tyr Glu Leu Gln Val Ala Glu Asp Gln Glu
      180              185              190

Glu Lys Gln Pro Gln Leu Ile Val Met Gly Asn Leu Asp Arg Glu Arg
      195              200              205

Trp Asp Ser Tyr Asp Leu Thr Ile Lys Val Gln Asp Gly Gly Ser Pro
      210              215              220

Pro Arg Ala Thr Ser Ala Leu Leu Arg Val Thr Val Leu Asp Thr Asn
      225              230              235              240

Asp Asn Ala Pro Lys Phe Glu Arg Pro Ser Tyr Glu Ala Glu Leu Ser
      245              250              255

Glu Asn Ser Pro Ile Gly His Ser Val Ile Gln Val Lys Ala Asn Asp
      260              265              270

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Ser | Asp | Gln | Gly | Ala | Asn | Ala | Glu | Ile | Glu | Tyr | Thr | Phe | His | Gln | Ala | | |
| | | 275 | | | | | 280 | | | | | 285 | | | | | |
| Pro | Glu | Val | Val | Arg | Arg | Leu | Leu | Arg | Leu | Asp | Arg | Asn | Thr | Gly | Leu | | |
| | | 290 | | | | 295 | | | | | 300 | | | | | | |
| Ile | Thr | Val | Gln | Gly | Pro | Val | Asp | Arg | Glu | Asp | Leu | Ser | Thr | Leu | Arg | | |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | | |
| Phe | Ser | Val | Leu | Ala | Lys | Asp | Arg | Gly | Thr | Asn | Pro | Lys | Ser | Ala | Arg | | |
| | | | | 325 | | | | | 330 | | | | | 335 | | | |
| Ala | Gln | Val | Val | Val | Thr | Val | Lys | Asp | Met | Asn | Asp | Asn | Ala | Pro | Thr | | |
| | | | 340 | | | | | 345 | | | | | 350 | | | | |
| Ile | Glu | Ile | Arg | Gly | Ile | Gly | Leu | Val | Thr | His | Gln | Asp | Gly | Met | Ala | | |
| | | 355 | | | | | 360 | | | | | 365 | | | | | |
| Asn | Ile | Ser | Glu | Asp | Val | Ala | Glu | Glu | Thr | Ala | Val | Ala | Leu | Val | Gln | | |
| | | 370 | | | | 375 | | | | | 380 | | | | | | |
| Val | Ser | Asp | Arg | Asp | Glu | Gly | Glu | Asn | Ala | Ala | Val | Thr | Cys | Val | Val | | |
| 385 | | | | | 390 | | | | 395 | | | | | 400 | | | |
| Ala | Gly | Asp | Val | Pro | Phe | Gln | Leu | Arg | Gln | Ala | Ser | Glu | Thr | Gly | Ser | | |
| | | | | 405 | | | | | 410 | | | | | 415 | | | |
| Asp | Ser | Lys | Lys | Lys | Tyr | Phe | Leu | Gln | Thr | Thr | Thr | Pro | Leu | Asp | Tyr | | |
| | | | 420 | | | | | 425 | | | | | 430 | | | | |
| Glu | Lys | Val | Lys | Asp | Tyr | Thr | Ile | Glu | Ile | Val | Ala | Val | Asp | Ser | Gly | | |
| | | 435 | | | | 440 | | | | | 445 | | | | | | |
| Asn | Pro | Pro | Leu | Ser | Ser | Thr | Asn | Ser | Leu | Lys | Val | Gln | Val | Val | Asp | | |
| | | 450 | | | | 455 | | | | | 460 | | | | | | |
| Val | Asn | Asp | Asn | Ala | Pro | Val | Phe | Thr | Gln | Ser | Val | Thr | Glu | Val | Ala | | |
| 465 | | | | | 470 | | | | | 475 | | | | | 480 | | |
| Phe | Pro | Glu | Asn | Asn | Lys | Pro | Gly | Glu | Val | Ile | Ala | Glu | Ile | Thr | Ala | | |
| | | | | 485 | | | | 490 | | | | | | 495 | | | |
| Ser | Asp | Ala | Asp | Ser | Gly | Ser | Asn | Ala | Glu | Leu | Val | Tyr | Ser | Leu | Glu | | |
| | | | 500 | | | | | 505 | | | | | 510 | | | | |
| Pro | Glu | Pro | Ala | Ala | Lys | Gly | Leu | Phe | Thr | Ile | Ser | Pro | Glu | Thr | Gly | | |
| | | 515 | | | | | 520 | | | | | 525 | | | | | |
| Glu | Ile | Gln | Val | Lys | Thr | Ser | Leu | Asp | Arg | Glu | Gln | Arg | Glu | Ser | Tyr | | |
| | | 530 | | | | 535 | | | | | 540 | | | | | | |
| Glu | Leu | Lys | Val | Val | Ala | Ala | Asp | Arg | Gly | Ser | Pro | Ser | Leu | Gln | Gly | | |
| 545 | | | | | 550 | | | | | 555 | | | | | 560 | | |
| Thr | Ala | Thr | Val | Leu | Val | Asn | Val | Leu | Asp | Cys | Asn | Asp | Asn | Asp | Pro | | |
| | | | | 565 | | | | | 570 | | | | | 575 | | | |
| Lys | Phe | Met | Leu | Ser | Gly | Tyr | Asn | Phe | Ser | Val | Met | Glu | Asn | Met | Pro | | |
| | | | 580 | | | | | 585 | | | | | 590 | | | | |

Ala Leu Ser Pro Val Gly Met Val Thr Val Ile Asp Gly Asp Lys Gly
595 600 605

Glu Asn Ala Gln Val Gln Leu Ser Val Glu Gln Asp Asn Gly Asp Phe
610 615 620

Val Ile Gln Asn Gly Thr Gly Thr Ile Leu Ser Ser Leu Ser Phe Asp
625 630 635 640

Arg Glu Gln Gln Ser Thr Tyr Thr Phe Gln Leu Lys Ala Val Asp Gly
645 650 655

Gly Val Pro Pro Arg Ser Ala Tyr Val Gly Val Thr Ile Asn Val Leu
660 665 670

Asp Glu Asn Asp Asn Ala Pro Tyr Ile Thr Ala Pro Ser Asn Thr Ser
675 680 685

His Lys Leu Leu Thr Pro Gln Thr Arg Leu Gly Glu Thr Val Ser Gln
690 695 700

Val Ala Ala Glu Asp Phe Asp Ser Gly Val Asn Ala Glu Leu Ile Tyr
705 710 715 720

Ser Ile Ala Gly Gly Asn Pro Tyr Gly Leu Phe Gln Ile Gly Ser His
725 730 735

Ser Gly Ala Ile Thr Leu Glu Lys Glu Ile Glu Arg Arg His His Gly
740 745 750

Leu His Arg Leu Val Val Lys Val Ser Asp Arg Gly Lys Pro Pro Arg
755 760 765

Tyr Gly Thr Ala Leu Val His Leu Tyr Val Asn Glu Thr Leu Ala Asn
770 775 780

Arg Thr Leu Leu Glu Thr Leu Leu Gly His Ser Leu Asp Thr Pro Leu
785 790 795 800

Asp Ile Asp Ile Ala Gly Asp Pro Glu Tyr Glu Arg Ser Lys Gln Arg
805 810 815

Gly Asn Ile Leu Phe Gly Val Val Ala Gly Val Val Ala Val Ala Leu
820 825 830

Leu Ile Ala Leu Ala Val Leu Val Arg Tyr Cys Arg Gln Arg Glu Ala
835 840 845

Lys Ser Gly Tyr Gln Ala Gly Lys Lys Glu Thr Lys Asp Leu Tyr Ala
850 855 860

Pro Lys Pro Ser Gly Lys Ala Ser Lys Gly Asn Lys Ser Lys Gly Lys
865 870 875 880

Lys Ser Lys Ser Pro Lys Pro Val Lys Pro Val Glu Asp Glu Asp Glu
885 890 895

Ala Gly Leu Gln Lys Ser Leu Lys Phe Asn Leu Met Ser Asp Ala Pro
900 905 910

Gly Asp Ser Pro Arg Ile His Leu Pro Leu Asn Tyr Pro Pro Gly Ser
 915 920 925

Pro Asp Leu Gly Arg His Tyr Arg Ser Asn Ser Pro Leu Pro Ser Ile
 930 935 940

Gln Leu Gln Pro Gln Ser Pro Ser Ala Ser Lys Lys His Gln Val Val
 945 950 955 960

Gln Asp Leu Pro Pro Ala Asn Thr Phe Val Gly Thr Gly Asp Thr Thr
 965 970 975

Ser Thr Gly Ser Glu Gln Tyr Ser Asp Tyr Ser Tyr Arg Thr Asn Pro
 980 985 990

Pro Lys Tyr Pro Ser Lys Gln Val Gly Gln Pro Phe Gln Leu Ser Thr
 995 1000 1005

Pro Gln Pro Leu Pro His Pro Tyr His Gly Ala Ile Trp Thr Glu Val
 1010 1015 1020

Trp Glu
 1025

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4705 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 115..2827

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

| | |
|---|----------|
| CGAAAGCCAT GTCGGACTCG TCGCCCAGCG CCCAAGCGCT AACCCGCTGA AAGTTTCTCA | 60 |
| GCGAAATCTC AGGGACGATC TGGACCCCGC TGAGAGGAAC TGCTTTTGAG TGAG ATG | 117 |
| | Met |
| | 1 |
| GTC CCA GAG GCC TGG AGG AGC GGA CTG GTA AGC ACC GGG AGG GTA GTG | 165 |
| Val Pro Glu Ala Trp Arg Ser Gly Leu Val Ser Thr Gly Arg Val Val | |
| | 5 10 15 |
| GGA GTT TTG CTT CTG CTT GGT GCC TTG AAC AAG GCT TCC ACG GTC ATT | 213 |
| Gly Val Leu Leu Leu Gly Ala Leu Asn Lys Ala Ser Thr Val Ile | |
| | 20 25 30 |
| CAC TAT GAG ATC CCG GAG GAA AGA GAG AAG GGT TTC GCT GTG GGC AAC | 261 |
| His Tyr Glu Ile Pro Glu Glu Arg Glu Lys Gly Phe Ala Val Gly Asn | |
| | 35 40 45 |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| GTG | GTC | GCG | AAC | CTT | GGT | TTG | GAT | CTC | GGT | AGC | CTC | TCA | GCC | CGC | AGG | 309 |
| Val | Val | Ala | Asn | Leu | Gly | Leu | Asp | Leu | Gly | Ser | Leu | Ser | Ala | Arg | Arg | |
| 50 | | | | | 55 | | | | | 60 | | | | | 65 | |
| TTC | CCG | GTG | GTG | TCT | GGA | GCT | AGC | CGA | AGA | TTC | TTT | GAG | GTG | AAC | CGG | 357 |
| Phe | Pro | Val | Val | Ser | Gly | Ala | Ser | Arg | Arg | Phe | Phe | Glu | Val | Asn | Arg | |
| | | | | 70 | | | | | 75 | | | | | 80 | | |
| GAG | ACC | GGA | GAG | ATG | TTT | GTG | AAC | GAC | CGT | CTG | GAT | CGA | GAG | GAG | CTG | 405 |
| Glu | Thr | Gly | Glu | Met | Phe | Val | Asn | Asp | Arg | Leu | Asp | Arg | Glu | Glu | Leu | |
| | | | 85 | | | | | 90 | | | | | 95 | | | |
| TGT | GGG | ACA | CTG | CCC | TCT | TGC | ACT | GTA | ACT | CTG | GAG | TTG | GTA | GTG | GAG | 453 |
| Cys | Gly | Thr | Leu | Pro | Ser | Cys | Thr | Val | Thr | Leu | Glu | Leu | Val | Val | Glu | |
| | | 100 | | | | | 105 | | | | | 110 | | | | |
| AAC | CCG | CTG | GAG | CTG | TTC | AGC | GTG | GAA | GTG | GTG | ATC | CAG | GAC | ATC | AAC | 501 |
| Asn | Pro | Leu | Glu | Leu | Phe | Ser | Val | Glu | Val | Val | Ile | Gln | Asp | Ile | Asn | |
| | 115 | | | | | 120 | | | | | 125 | | | | | |
| GAC | AAC | AAT | CCT | GCT | TTC | CCT | ACC | CAG | GAA | ATG | AAA | TTG | GAG | ATT | AGC | 549 |
| Asp | Asn | Asn | Pro | Ala | Phe | Pro | Thr | Gln | Glu | Met | Lys | Leu | Glu | Ile | Ser | |
| 130 | | | | | 135 | | | | | 140 | | | | | 145 | |
| GAG | GCC | GTG | GCT | CCG | GGG | ACG | CGC | TTT | CCG | CTC | GAG | AGC | GCG | CAC | GAT | 597 |
| Glu | Ala | Val | Ala | Pro | Gly | Thr | Arg | Phe | Pro | Leu | Glu | Ser | Ala | His | Asp | |
| | | | | 150 | | | | | 155 | | | | | 160 | | |
| CCC | GAT | CTG | GGA | AGC | AAC | TCT | TTA | CAA | ACC | TAT | GAG | CTG | AGC | CGA | AAT | 645 |
| Pro | Asp | Leu | Gly | Ser | Asn | Ser | Leu | Gln | Thr | Tyr | Glu | Leu | Ser | Arg | Asn | |
| | | | 165 | | | | | 170 | | | | | 175 | | | |
| GAA | TAC | TTT | GCG | CTT | CGC | GTG | CAG | ACG | CGG | GAG | GAC | AGC | ACC | AAG | TAC | 693 |
| Glu | Tyr | Phe | Ala | Leu | Arg | Val | Gln | Thr | Arg | Glu | Asp | Ser | Thr | Lys | Tyr | |
| | | 180 | | | | | 185 | | | | | 190 | | | | |
| GCG | GAG | CTG | GTG | TTG | GAG | CGC | GCC | CTG | GAC | CGA | GAA | CGG | GAG | CCT | AGT | 741 |
| Ala | Glu | Leu | Val | Leu | Glu | Arg | Ala | Leu | Asp | Arg | Glu | Arg | Glu | Pro | Ser | |
| | 195 | | | | | 200 | | | | | 205 | | | | | |
| CTC | CAG | TTA | GTG | CTG | ACG | GCG | TTG | GAC | GGA | GGG | ACC | CCA | GCT | CTC | TCC | 789 |
| Leu | Gln | Leu | Val | Leu | Thr | Ala | Leu | Asp | Gly | Gly | Thr | Pro | Ala | Leu | Ser | |
| 210 | | | | | 215 | | | | | 220 | | | | | 225 | |
| GCC | AGC | CTG | CCT | ATT | CAC | ATC | AAG | GTG | CTG | GAC | GCG | AAT | GAC | AAT | GCG | 837 |
| Ala | Ser | Leu | Pro | Ile | His | Ile | Lys | Val | Leu | Asp | Ala | Asn | Asp | Asn | Ala | |
| | | | 230 | | | | | | 235 | | | | | 240 | | |
| CCT | GTC | TTC | AAC | CAG | TCC | TTG | TAC | CGG | GCG | CGC | GTT | CCT | GGA | GGA | TGC | 885 |
| Pro | Val | Phe | Asn | Gln | Ser | Leu | Tyr | Arg | Ala | Arg | Val | Pro | Gly | Gly | Cys | |
| | | | 245 | | | | | 250 | | | | | 255 | | | |
| ACC | TCC | GGC | ACG | CGC | GTG | GTA | CAA | GTC | CTT | GCA | ACG | GAT | CTG | GAT | GAA | 933 |
| Thr | Ser | Gly | Thr | Arg | Val | Val | Gln | Val | Leu | Ala | Thr | Asp | Leu | Asp | Glu | |
| | | 260 | | | | | 265 | | | | | 270 | | | | |
| GGC | CCC | AAC | GGT | GAA | ATT | ATT | TAC | TCC | TTC | GGC | AGC | CAC | AAC | CGC | GCC | 981 |
| Gly | Pro | Asn | Gly | Glu | Ile | Ile | Tyr | Ser | Phe | Gly | Ser | His | Asn | Arg | Ala | |
| | 275 | | | | | 280 | | | | | 285 | | | | | |

| | | | | | | | | | | | | | | | | |
|-------------------|------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| GGC Gly 290 | GTG Val | CGG Arg | CAA Gln | CTA Leu | TTC Phe 295 | GCC Ala | TTA Leu | GAC Asp | CTT Leu | GTA Val 300 | ACC Thr | GGG Gly | ATG Met | CTG Leu | ACA Thr 305 | 1029 |
| ATC Ile | AAG Lys | GGT Gly | CGG Arg | CTG Leu 310 | GAC Asp | TTC Phe | GAG Glu | GAC Asp | ACC Thr 315 | AAA Lys | CTC Leu | CAT His | GAG Glu | ATT Ile 320 | TAC Tyr | 1077 |
| ATC Ile | CAG Gln | GCC Ala | AAA Lys 325 | GAC Asp | AAG Lys | GGC Gly | GCC Ala | AAT Asn 330 | CCC Pro | GAA Glu | GGA Gly | GCA Ala | CAT His 335 | TGC Cys | AAA Lys | 1125 |
| GTG Val | TTG Leu | GTG Val 340 | GAG Glu | GTT Val | GTG Val | GAT Asp | GTG Val 345 | AAT Asn | GAC Asp | AAC Asn | GCC Ala | CCG Pro 350 | GAG Glu | ATC Ile | ACA Thr | 1173 |
| GTC Val 355 | ACC Thr | TCC Ser | GTG Val | TAC Tyr | AGC Ser | CCA Pro 360 | GTA Val | CCC Pro | GAG Glu | GAT Asp | GCC Ala 365 | TCT Ser | GGG Gly | ACT Thr | GTC Val | 1221 |
| ATC Ile 370 | GCT Ala | TTG Leu | CTC Leu | AGT Ser | GTG Val 375 | ACT Thr | GAC Asp | CTG Leu | GAT Asp | GCT Ala 380 | GGC Gly | GAG Glu | AAC Asn | GGG Gly 385 | CTG Leu | 1269 |
| GTG Val | ACC Thr | TGC Cys | GAA Glu | GTT Val 390 | CCA Pro | CCG Pro | GGT Gly | CTC Leu | CCT Pro 395 | TTC Phe | AGC Ser | CTT Leu | ACT Thr | TCT Ser 400 | TCC Ser | 1317 |
| CTC Leu | AAG Lys | AAT Asn | TAC Tyr 405 | TTC Phe | ACT Thr | TTG Leu | AAA Lys | ACC Thr 410 | AGT Ser | GCA Ala | GAC Asp | CTG Leu | GAT Asp 415 | CGG Arg | GAG Glu | 1365 |
| ACT Thr | GTG Val | CCA Pro 420 | GAA Glu | TAC Tyr | AAC Asn | CTC Leu | AGC Ser 425 | ATC Ile | ACC Thr | GCC Ala | CGA Arg | GAC Asp 430 | GCC Ala | GGA Gly | ACC Thr | 1413 |
| CCT Pro 435 | TCC Ser | CTC Leu | TCA Ser | GCC Ala | CTT Leu | ACA Thr 440 | ATA Ile | GTG Val | CGT Arg | GTT Val | CAA Gln 445 | GTG Val | TCC Ser | GAC Asp | ATC Ile | 1461 |
| AAT Asn 450 | GAC Asp | AAC Asn | CCT Pro | CCA Pro | CAA Gln 455 | TCT Ser | TCT Ser | CAA Gln | TCT Ser | TCC Ser 460 | TAC Tyr | GAC Asp | GTT Val | TAC Tyr 465 | ATT Ile | 1509 |
| GAA Glu | GAA Glu | AAC Asn | AAC Asn | CTC Leu 470 | CCC Pro | GGG Gly | GCT Ala | CCA Pro 475 | ATA Ile | CTA Leu | AAC Asn | CTA Leu | AGT Ser | GTC Val 480 | TGG Trp | 1557 |
| GAC Asp | CCC Pro | GAC Asp | GCC Ala 485 | CCG Pro | CAG Gln | AAT Asn | GCT Ala 490 | CGG Arg | CTT Leu | TCT Ser | TTC Phe | TTT Phe | CTC Leu 495 | TTG Leu | GAG Glu | 1605 |
| CAA Gln | GGA Gly | GCT Ala 500 | GAA Glu | ACC Thr | GGG Gly | CTA Leu | GTG Val 505 | GGT Gly | CGC Arg | TAT Tyr | TTC Phe | ACA Thr 510 | ATA Ile | AAT Asn | CGT Arg | 1653 |
| GAC Asp 515 | AAT Asn | GGC Gly | ATA Ile | GTG Val | TCA Ser | TCC Ser 520 | TTA Leu | GTG Val | CCC Pro | CTA Leu | GAC Asp 525 | TAT Tyr | GAG Glu | GAT Asp | CGG Arg | 1701 |

| | | | | | | | | | | | | | | | | |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| CGG Arg 530 | GAA Glu | TTT Phe | GAA Glu | TTA Leu | ACA Thr 535 | GCT Ala | CAT His | ATC Ile | AGC Ser | GAT Asp 540 | GGG Gly | GGC Gly | ACC Thr | CCG Pro | GTC Val 545 | 1749 |
| CTA Leu | GCC Ala | ACC Thr | AAC Asn | ATC Ile 550 | AGC Ser | GTG Val | AAC Asn | ATA Ile | TTT Phe 555 | GTC Val | ACT Thr | GAT Asp | CGC Arg | AAT Asn 560 | GAC Asp | 1797 |
| AAT Asn | GCC Ala | CCC Pro | CAG Gln 565 | GTC Val | CTA Leu | TAT Tyr | CCT Pro | CGG Arg 570 | CCA Pro | GGT Gly | GGG Gly | AGC Ser | TCG Ser 575 | GTG Val | GAG Glu | 1845 |
| ATG Met | CTG Leu | CCT Pro 580 | CGA Arg | GGT Gly | ACC Thr | TCA Ser | GCT Ala 585 | GGC Gly | CAC His | CTA Leu | GTG Val | TCA Ser | CGG Arg 590 | GTG Val | GTA Val | 1893 |
| GGC Gly | TGG Trp 595 | GAC Asp | GCG Ala | GAT Asp | GCA Ala | GGG Gly 600 | CAC His | AAT Asn | GCC Ala | TGG Trp | CTC Leu 605 | TCC Ser | TAC Tyr | AGT Ser | CTC Leu | 1941 |
| TTT Phe 610 | GGA Gly | TCC Ser | CCT Pro | AAC Asn | CAG Gln 615 | AGC Ser | CTT Leu | TTT Phe | GCC Ala 620 | ATA Ile | GGG Gly | CTG Leu | CAC His | ACT Thr | GGT Gly 625 | 1989 |
| CAA Gln | ATC Ile | AGT Ser | ACT Thr | GCC Ala 630 | CGT Arg | CCA Pro | GTC Val | CAA Gln | GAC Asp 635 | ACA Thr | GAT Asp | TCA Ser | CCC Pro | AGG Arg 640 | CAG Gln | 2037 |
| ACT Thr | CTC Leu | ACT Thr | GTC Val 645 | TTG Leu | ATC Ile | AAA Lys | GAC Asp | AAT Asn 650 | GGG Gly | GAG Glu | CCT Pro | TCG Ser | CTC Leu 655 | TCC Ser | ACC Thr | 2085 |
| ACT Thr | GCT Ala | ACC Thr 660 | CTC Leu | ACT Thr | GTG Val | TCA Ser | GTA Val 665 | ACC Thr | GAG Glu | GAC Asp | TCT Ser | CCT Pro | GAA Glu 670 | GCC Ala | CGA Arg | 2133 |
| GCC Ala | GAG Glu 675 | TTC Phe | CCC Pro | TCT Ser | GGC Gly | TCT Ser 680 | GCC Ala | CCC Pro | CGG Arg | GAG Glu | CAG Gln 685 | AAA Lys | AAA Lys | AAT Asn | CTC Leu | 2181 |
| ACC Thr 690 | TTT Phe | TAT Tyr | CTA Leu | CTT Leu | CTT Leu 695 | TCT Ser | CTA Leu | ATC Ile | CTG Leu | GTT Val 700 | TCT Ser | GTG Val | GGC Gly | TTC Phe | GTG Val 705 | 2229 |
| GTC Val | ACA Thr | GTG Val | TTC Phe | GGA Gly 710 | GTA Val | ATC Ile | ATA Ile | TTC Phe | AAA Lys 715 | GTT Val | TAC Tyr | AAG Lys | TGG Trp 720 | AAG Lys | CAG Gln | 2277 |
| TCT Ser | AGA Arg | GAC Asp | CTA Leu 725 | TAC Tyr | CGA Arg | GCC Ala | CCG Pro | GTG Val 730 | AGC Ser | TCA Ser | CTG Leu | TAC Tyr | CGA Arg 735 | ACA Thr | CCA Pro | 2325 |
| GGG Gly | CCC Pro | TCC Ser 740 | TTG Leu | CAC His | GCG Ala | GAC Asp | GCC Ala 745 | GTG Val | CGG Arg | GGA Gly | GGC Gly | CTG Leu 750 | ATG Met | TCG Ser | CCG Pro | 2373 |
| CAC His 755 | CTT Leu | TAC Tyr | CAT His | CAG Gln | GTG Val | TAT Tyr 760 | CTC Leu | ACC Thr | ACG Thr | GAC Asp | TCC Ser 765 | CGC Arg | CGC Arg | AGC Ser | GAC Asp | 2421 |

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|---|------|
| CCG CTG CTG AAG AAA CCT GGT GCA GCC AGT CCA CTG GCC AGC CGC CAG Pro Leu Leu Lys Lys Pro Gly Ala Ala Ser Pro Leu Ala Ser Arg Gln 770 775 780 785 | 2469 |
| AAC ACG CTG CGG AGC TGT GAT CCG GTG TTC TAT AGG CAG GTG TTG GGT Asn Thr Leu Arg Ser Cys Asp Pro Val Phe Tyr Arg Gln Val Leu Gly 790 795 800 | 2517 |
| GCA GAG AGC GCC CCT CCC GGA CAG CAA GCC CCG CCC AAC ACG GAC TGG Ala Glu Ser Ala Pro Pro Gly Gln Gln Ala Pro Pro Asn Thr Asp Trp 805 810 815 | 2565 |
| CGT TTC TCT CAG GCC CAG AGA CCC GGC ACC AGC GGC TCC CAA AAT GGC Arg Phe Ser Gln Ala Gln Arg Pro Gly Thr Ser Gly Gln Asn Gly 820 825 830 | 2613 |
| GAT GAC ACC GGC ACC TGG CCC AAC AAC CAG TTT GAC ACA GAG ATG CTG Asp Asp Thr Gly Thr Trp Pro Asn Asn Gln Phe Asp Thr Glu Met Leu 835 840 845 | 2661 |
| CAA GCC ATG ATC TTG GCG TCC GCC AGT GAA GCT GCT GAT GGG AGC TCC Gln Ala Met Ile Leu Ala Ser Ala Ser Glu Ala Ala Asp Gly Ser Ser 850 855 860 865 | 2709 |
| ACC CTG GGA GGG GGT GCC GGC ACC ATG GGA TTG AGC GCC CGC TAC GGA Thr Leu Gly Gly Gly Ala Gly Thr Met Gly Leu Ser Ala Arg Tyr Gly 870 875 880 | 2757 |
| CCC CAG TTC ACC CTG CAG CAC GTG CCC GAC TAC CGC CAG AAT GTC TAC Pro Gln Phe Thr Leu Gln His Val Pro Asp Tyr Arg Gln Asn Val Tyr 885 890 895 | 2805 |
| ATC CCA GGC AGC AAT GCA CAC T GACCAACGCA GCTGGCAAGC GGATGGCAAG Ile Pro Gly Ser Asn Ala His 900 | 2857 |
| CCCCAGCAGG TGGCAATGGC AACAAGAAGA AGTCGGCAAG AAGGAGAAGA AGTAACATGG | 2917 |
| AGGCCAGGCC AAGAGCCACA GGGCAGCCTC TCCCCGAACC AGCCCAGCTT CTCCTTACCT | 2977 |
| GCACCCAGGC CTCAGAGTTT CAGGGCTAAC CCCCAGAATA CTGGTAGGGG CCAAGGCATC | 3037 |
| TCCCTTGGA ACAGAAACAA GTGCCATCAC ACCATCCCTT CCCCAGGTGT AATATCCAAA | 3097 |
| GCAGTTCCGC TGGGAACCCC ATCCAATCAG TGGCTGTACC CATTTGGGTA GTGGGGTTCA | 3157 |
| TGTAGACACC AAGAACCATT TGCCACACCC CGTTTAGTTA CAGCTGAACC CTCCATCTTC | 3217 |
| CAAATCAATC AGGCCCATCC ATCCCATGCC TCCCTCCTCC CCACCCCACT CCAACAGTTC | 3277 |
| CTCTTTCCCG AGTAAGGTGG TTGGGGTGTT GAAGTACCAA GTAACCTACA AGCCTCCTAG | 3337 |
| TTCTGAAAAG TTGGAAGGGC ATCATGACCT CTTGGCCTCT CCTTTGATTC TCAATCTTCC | 3397 |
| CCCAAAGCAT GGTTTGGTGC CAGCCCCCTC ACCTCCTTCC AGAGCCCAAG ATCAATGCTC | 3457 |
| AAGTTTTGGA GGACATGATC ACCATCCCCA TGGTACTGAT GCTTGCTGGA TTTAGGGAGG | 3517 |
| GCATTTTGCT ACCAAGCCTC TTCCCAACGC CCTGGGACCA GTCTTCTGTT TTGTTTTTCA | 3577 |
| TTGTTTGAGC TTTCCACTGC ATGCCTTGAC TTCCCCCACC TCCTCCTCAA ACAAGAGACT | 3637 |

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|--|------|
| CCACTGCATG TTCCAAGACA GTATGGGGTG GTAAGATAAG GAAGGGAAGT GTGTGGATGT | 3697 |
| GGATGGTGGG GGCATGGACA AAGCTTGACA CATCAAGTTA TCAAGGCCTT GGAGGAGGCT | 3757 |
| CTGTATGTCC TCAGGGGACT GACAACATCC TCCAGATTCC AGCCATAAAC CAATAACTAG | 3817 |
| GCTGGACCCT TCCCACTACA TAATAGGGCT CAGCCAGGCA GCCAGCTTTG GGCTGAGCTA | 3877 |
| ACAGGACCAA TGGATTAACT GGCATTTTCAG TCCAAGGAAG CTCGAAGCAG GTTTAGGACC | 3937 |
| AGGTCCCCCTT GAGAGGTCAG AGGGGCCTCT GTGGGTGCTG GGTACTCCAG AGGTGCCACT | 3997 |
| GGTGAAGGG TCAGCGGAGC CCCAGCAGGA AGGGTGGGCC AGCCAGGCCA TTCTTAGTCC | 4057 |
| CTGGGTGGG GAGGCAGGA GCTAGGGCAG GGACCAAATG AACAGAAAGT CTCAGCCCAG | 4117 |
| GATGGGGCTT CTTCAACAGG CCCCTGCCCT CCTGAAGCCT CAGTCCTTCA CCTTGCCAGG | 4177 |
| TGCCGTTTCT CTTCCGTGAA GGCCACTGCC CAGGTCCCCA GTGCGCCCCC TAGTGGCCAT | 4237 |
| AGCCTGGTTA AAGTTCCCCA GTGCCTCCTT GTGATAGACC TTCTTCTCCC ACCCCCTTCT | 4297 |
| GCCCCTGGGT CCCCGGCCAT CCAGCGGGGC TGCCAGAGAA CCCAGACCT GCCCTTACAG | 4357 |
| TAGTGTAGCG CCCCTCCCT CTTTCGGCTG GTGTAGAATA GCCAGTAGTG TAGTGCGGTG | 4417 |
| TGCTTTTACG TGATGGCGGG TGGGCAGCGG GCGGCGGCGT CCGCGCAGCC GTCTGTCTT | 4477 |
| GATCTGCCCC CGGCGGCCCC TGTGTGTGTT TGTGCTGTGT CCAGCGCTAA GGCGACCCCC | 4537 |
| TCCCCCGTAC TGACTTCTCC TATAAGCGCT TCTCTTCGCA TAGTCACGTA GCTCCCACCC | 4597 |
| CACCCTCTTC CTGTGTCTCA CGCAAGTTT ATACTCTAAT ATTTATATGG CTTTTTTTCT | 4657 |
| TCGACAAAAA AATAATAAAA CGTTTCTTCT GAAAAAAAAA AAAAAAAA | 4705 |

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 904 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

| | |
|---|--|
| Met Val Pro Glu Ala Trp Arg Ser Gly Leu Val Ser Thr Gly Arg Val | |
| 1 5 10 15 | |
| Val Gly Val Leu Leu Leu Gly Ala Leu Asn Lys Ala Ser Thr Val | |
| 20 25 30 | |
| Ile His Tyr Glu Ile Pro Glu Glu Arg Glu Lys Gly Phe Ala Val Gly | |
| 35 40 45 | |
| Asn Val Val Ala Asn Leu Gly Leu Asp Leu Gly Ser Leu Ser Ala Arg | |
| 50 55 60 | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Arg | Phe | Pro | Val | Val | Ser | Gly | Ala | Ser | Arg | Arg | Phe | Phe | Glu | Val | Asn | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | |
| Arg | Glu | Thr | Gly | Glu | Met | Phe | Val | Asn | Asp | Arg | Leu | Asp | Arg | Glu | Glu | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| Leu | Cys | Gly | Thr | Leu | Pro | Ser | Cys | Thr | Val | Thr | Leu | Glu | Leu | Val | Val | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| Glu | Asn | Pro | Leu | Glu | Leu | Phe | Ser | Val | Glu | Val | Val | Ile | Gln | Asp | Ile | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| Asn | Asp | Asn | Asn | Pro | Ala | Phe | Pro | Thr | Gln | Glu | Met | Lys | Leu | Glu | Ile | |
| | 130 | | | | | 135 | | | | | 140 | | | | | |
| Ser | Glu | Ala | Val | Ala | Pro | Gly | Thr | Arg | Phe | Pro | Leu | Glu | Ser | Ala | His | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| Asp | Pro | Asp | Leu | Gly | Ser | Asn | Ser | Leu | Gln | Thr | Tyr | Glu | Leu | Ser | Arg | |
| | | | 165 | | | | | | 170 | | | | | 175 | | |
| Asn | Glu | Tyr | Phe | Ala | Leu | Arg | Val | Gln | Thr | Arg | Glu | Asp | Ser | Thr | Lys | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| Tyr | Ala | Glu | Leu | Val | Leu | Glu | Arg | Ala | Leu | Asp | Arg | Glu | Arg | Glu | Pro | |
| | | 195 | | | | | 200 | | | | | 205 | | | | |
| Ser | Leu | Gln | Leu | Val | Leu | Thr | Ala | Leu | Asp | Gly | Gly | Thr | Pro | Ala | Leu | |
| | 210 | | | | | 215 | | | | | 220 | | | | | |
| Ser | Ala | Ser | Leu | Pro | Ile | His | Ile | Lys | Val | Leu | Asp | Ala | Asn | Asp | Asn | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | |
| Ala | Pro | Val | Phe | Asn | Gln | Ser | Leu | Tyr | Arg | Ala | Arg | Val | Pro | Gly | Gly | |
| | | | | 245 | | | | | 250 | | | | | 255 | | |
| Cys | Thr | Ser | Gly | Thr | Arg | Val | Val | Gln | Val | Leu | Ala | Thr | Asp | Leu | Asp | |
| | | | 260 | | | | | 265 | | | | | 270 | | | |
| Glu | Gly | Pro | Asn | Gly | Glu | Ile | Ile | Tyr | Ser | Phe | Gly | Ser | His | Asn | Arg | |
| | | 275 | | | | | 280 | | | | | 285 | | | | |
| Ala | Gly | Val | Arg | Gln | Leu | Phe | Ala | Leu | Asp | Leu | Val | Thr | Gly | Met | Leu | |
| | 290 | | | | | 295 | | | | | 300 | | | | | |
| Thr | Ile | Lys | Gly | Arg | Leu | Asp | Phe | Glu | Asp | Thr | Lys | Leu | His | Glu | Ile | |
| 305 | | | | | 310 | | | | | 315 | | | | 320 | | |
| Tyr | Ile | Gln | Ala | Lys | Asp | Lys | Gly | Ala | Asn | Pro | Glu | Gly | Ala | His | Cys | |
| | | | | 325 | | | | | 330 | | | | | 335 | | |
| Lys | Val | Leu | Val | Glu | Val | Val | Asp | Val | Asn | Asp | Asn | Ala | Pro | Glu | Ile | |
| | | | 340 | | | | | 345 | | | | | 350 | | | |
| Thr | Val | Thr | Ser | Val | Tyr | Ser | Pro | Val | Pro | Glu | Asp | Ala | Ser | Gly | Thr | |
| | | 355 | | | | | 360 | | | | | 365 | | | | |
| Val | Ile | Ala | Leu | Leu | Ser | Val | Thr | Asp | Leu | Asp | Ala | Gly | Glu | Asn | Gly | |
| | 370 | | | | | 375 | | | | | 380 | | | | | |

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Val | Thr | Cys | Glu | Val | Pro | Pro | Gly | Leu | Pro | Phe | Ser | Leu | Thr | Ser | 385 | 390 | 395 | 400 |
| Ser | Leu | Lys | Asn | Tyr | Phe | Thr | Leu | Lys | Thr | Ser | Ala | Asp | Leu | Asp | Arg | 405 | 410 | 415 | |
| Glu | Thr | Val | Pro | Glu | Tyr | Asn | Leu | Ser | Ile | Thr | Ala | Arg | Asp | Ala | Gly | 420 | 425 | 430 | |
| Thr | Pro | Ser | Leu | Ser | Ala | Leu | Thr | Ile | Val | Arg | Val | Gln | Val | Ser | Asp | 435 | 440 | 445 | |
| Ile | Asn | Asp | Asn | Pro | Pro | Gln | Ser | Ser | Gln | Ser | Ser | Tyr | Asp | Val | Tyr | 450 | 455 | 460 | |
| Ile | Glu | Glu | Asn | Asn | Leu | Pro | Gly | Ala | Pro | Ile | Leu | Asn | Leu | Ser | Val | 465 | 470 | 475 | 480 |
| Trp | Asp | Pro | Asp | Ala | Pro | Gln | Asn | Ala | Arg | Leu | Ser | Phe | Phe | Leu | Leu | 485 | 490 | 495 | |
| Glu | Gln | Gly | Ala | Glu | Thr | Gly | Leu | Val | Gly | Arg | Tyr | Phe | Thr | Ile | Asn | 500 | 505 | 510 | |
| Arg | Asp | Asn | Gly | Ile | Val | Ser | Ser | Leu | Val | Pro | Leu | Asp | Tyr | Glu | Asp | 515 | 520 | 525 | |
| Arg | Arg | Glu | Phe | Glu | Leu | Thr | Ala | His | Ile | Ser | Asp | Gly | Gly | Thr | Pro | 530 | 535 | 540 | |
| Val | Leu | Ala | Thr | Asn | Ile | Ser | Val | Asn | Ile | Phe | Val | Thr | Asp | Arg | Asn | 545 | 550 | 555 | 560 |
| Asp | Asn | Ala | Pro | Gln | Val | Leu | Tyr | Pro | Arg | Pro | Gly | Gly | Ser | Ser | Val | 565 | 570 | 575 | |
| Glu | Met | Leu | Pro | Arg | Gly | Thr | Ser | Ala | Gly | His | Leu | Val | Ser | Arg | Val | 580 | 585 | 590 | |
| Val | Gly | Trp | Asp | Ala | Asp | Ala | Gly | His | Asn | Ala | Trp | Leu | Ser | Tyr | Ser | 595 | 600 | 605 | |
| Leu | Phe | Gly | Ser | Pro | Asn | Gln | Ser | Leu | Phe | Ala | Ile | Gly | Leu | His | Thr | 610 | 615 | 620 | |
| Gly | Gln | Ile | Ser | Thr | Ala | Arg | Pro | Val | Gln | Asp | Thr | Asp | Ser | Pro | Arg | 625 | 630 | 635 | 640 |
| Gln | Thr | Leu | Thr | Val | Leu | Ile | Lys | Asp | Asn | Gly | Glu | Pro | Ser | Leu | Ser | 645 | 650 | 655 | |
| Thr | Thr | Ala | Thr | Leu | Thr | Val | Ser | Val | Thr | Glu | Asp | Ser | Pro | Glu | Ala | 660 | 665 | 670 | |
| Arg | Ala | Glu | Phe | Pro | Ser | Gly | Ser | Ala | Pro | Arg | Glu | Gln | Lys | Lys | Asn | 675 | 680 | 685 | |
| Leu | Thr | Phe | Tyr | Leu | Leu | Leu | Ser | Leu | Ile | Leu | Val | Ser | Val | Gly | Phe | 690 | 695 | 700 | |

Val Val Thr Val Phe Gly Val Ile Ile Phe Lys Val Tyr Lys Trp Lys
705 710 715 720

Gln Ser Arg Asp Leu Tyr Arg Ala Pro Val Ser Ser Leu Tyr Arg Thr
725 730 735

Pro Gly Pro Ser Leu His Ala Asp Ala Val Arg Gly Gly Leu Met Ser
740 745 750

Pro His Leu Tyr His Gln Val Tyr Leu Thr Thr Asp Ser Arg Arg Ser
755 760 765

Asp Pro Leu Leu Lys Lys Pro Gly Ala Ala Ser Pro Leu Ala Ser Arg
770 775 780

Gln Asn Thr Leu Arg Ser Cys Asp Pro Val Phe Tyr Arg Gln Val Leu
785 790 795 800

Gly Ala Glu Ser Ala Pro Pro Gly Gln Gln Ala Pro Pro Asn Thr Asp
805 810 815

Trp Arg Phe Ser Gln Ala Gln Arg Pro Gly Thr Ser Gly Ser Gln Asn
820 825 830

Gly Asp Asp Thr Gly Thr Trp Pro Asn Asn Gln Phe Asp Thr Glu Met
835 840 845

Leu Gln Ala Met Ile Leu Ala Ser Ala Ser Glu Ala Ala Asp Gly Ser
850 855 860

Ser Thr Leu Gly Gly Gly Ala Gly Thr Met Gly Leu Ser Ala Arg Tyr
865 870 875 880

Gly Pro Gln Phe Thr Leu Gln His Val Pro Asp Tyr Arg Gln Asn Val
885 890 895

Tyr Ile Pro Gly Ser Asn Ala His
900

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 556 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Asp Trp Val Ile Pro Pro Ile Asn Leu Pro Glu Asn Ser Arg Gly Pro
1 5 10 15

Phe Pro Gln Glu Leu Val Arg Ile Arg Ser Asp Arg Asp Lys Asn Leu
20 25 30

Ser Leu Arg Tyr Thr Val Thr Gly Pro Gly Ala Asp Gln Pro Pro Thr
35 40 45

Gly Ile Phe Ile Ile Asn Pro Ile Ser Gly Gln Leu Ser Val Thr Lys
50 55 60

Pro Leu Asp Arg Glu Gln Ile Ala Arg Phe His Leu Arg Ala His Ala
65 70 75 80

Val Asp Ile Asn Gly Asn Gln Val Glu Asn Pro Ile Asp Ile Val Ile
85 90 95

Asn Val Ile Asp Met Asn Asp Asn Arg Pro Glu Phe Leu His Gln Val
100 105 110

Trp Asn Gly Ser Val Pro Glu Gly Ser Lys Pro Gly Thr Tyr Val Met
115 120 125

Thr Val Thr Ala Ile Asp Ala Asp Asp Pro Asn Ala Leu Asn Gly Met
130 135 140

Leu Arg Tyr Arg Ile Leu Ser Gln Ala Pro Ser Thr Pro Ser Pro Asn
145 150 155 160

Met Phe Thr Ile Asn Asn Glu Thr Gly Asp Ile Ile Thr Val Ala Ala
165 170 175

Gly Leu Asp Arg Glu Lys Val Gln Gln Tyr Thr Leu Ile Ile Gln Ala
180 185 190

Thr Asp Met Glu Gly Asn Pro Thr Tyr Gly Leu Ser Asn Thr Ala Thr
195 200 205

Ala Val Ile Thr Val Thr Asp Val Asn Asp Asn Pro Pro Glu Phe Thr
210 215 220

Ala Met Thr Phe Tyr Gly Glu Val Pro Glu Asn Arg Val Asp Ile Ile
225 230 235 240

Val Ala Asn Leu Thr Val Thr Asp Lys Asp Gln Pro His Thr Pro Ala
245 250 255

Trp Asn Ala Val Thr Arg Ile Ser Gly Gly Asp Pro Thr Gly Arg Phe
260 265 270

Ala Ile Gln Thr Asp Pro Asn Ser Asn Asp Gly Leu Val Thr Val Val
275 280 285

Lys Pro Ile Asp Phe Glu Thr Asn Arg Met Phe Val Leu Thr Val Ala
290 295 300

Ala Glu Asn Gln Val Pro Leu Ala Lys Gly Ile Gln His Pro Pro Gln
305 310 315 320

Ser Thr Ala Thr Val Ser Val Thr Val Ile Asp Val Asn Glu Asn Pro
325 330 335

Tyr Phe Ala Pro Asn Pro Lys Ile Ile Arg Gln Glu Glu Gly Leu His
340 345 350

Ala Gly Thr Met Leu Thr Thr Phe Thr Ala Gly Asp Pro Asp Arg Tyr
355 360 365

Met Gln Gln Asn Ile Arg Tyr Thr Lys Leu Ser Asp Pro Ala Asn Trp
370 375 380

Leu Lys Ile Asp Pro Val Asn Gly Gln Ile Thr Thr Ile Ala Val Leu
385 390 395 400

Asp Arg Glu Ser Pro Asn Val Lys Asn Asn Ile Tyr Asn Ala Thr Phe
405 410 415

/ Leu Ala Ser Asp Asn Gly Ile Pro Pro Met Ser Gly Thr Gly Thr Leu
420 425 430

Gln Ile Tyr Leu Leu Asp Ile Asn Asp Asn Ala Pro Gln Val Leu Pro
435 440 445

Gln Glu Ala Glu Thr Cys Glu Thr Pro Asp Pro Asn Ser Ile Asn Ile
450 455 460

Thr Thr Ala Leu Asp Tyr Asp Ile Asp Pro Asn Ala Gly Pro Phe Ala
465 470 475 480

Tyr Asp Leu Pro Leu Ser Pro Val Thr Ile Lys Arg Asn Trp Thr Ile
485 490 495

Thr Arg Leu Asn Gly Asp Phe Ala Gln Leu Asn Leu Lys Ile Lys Phe
500 505 510

Leu Glu Ala Gly Ile Tyr Glu Val Pro Ile Ile Ile Thr Asp Ser Gly
515 520 525

Asn Pro Pro Lys Ser Asn Lys Ser Ile Leu Arg Val Arg Val Cys Gln
530 535 540

Cys Asp Phe Asn Gly Asp Cys Thr Asp Val Asp Arg
545 550 555

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 105 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Glu Asp Thr Val Tyr Ser Phe Asp Ile Pro Glu Asn Ala Gln Arg Gly
1 5 10 15

Tyr Gln Val Gly Gln Ile Val Ala Arg Asp Ala Asp Leu Gly Gln Asn
20 25 30

Ala Gln Leu Ser Tyr Gly Val Val Ser Asp Trp Ala Asn Asp Val Phe
35 40 45

Ser Leu Asn Pro Gln Thr Gly Met Leu Thr Leu Thr Ala Arg Leu Asp
50 55 60
Tyr Glu Glu Val Gln His Tyr Ile Leu Ile Val Gln Ala Gln Asp Asn
65 70 75 80
Gly Gln Pro Ser Leu Ser Thr Thr Ile Thr Val Tyr Cys Asn Val Leu
85 90 95
Asp Leu Asn Asp Asn Ala Pro Ile Phe
100 105

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Asp Xaa Asp Xaa Gly Xaa Asn
1 5

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

Ala Xaa Asp Xaa Gly Xaa Pro
1 5

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4650 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 495..4103

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

| | |
|--|------|
| CCTCTATTTCG ACATTCTCTT TGGATTGTTT TGCTATAACT TGAAATTTGG GATGTCACAA | 60 |
| ACGAAACTGT CATCTGTTTC CGCCAAACTG TGGTTCTGCT AATCTCCCAG GCTGGCAGCA | 120 |
| TTGGAGACTT GCTGACTTCT TTCATCCCCC ACTCTTTTCA CCTGAAATTC CTTTCCTTGG | 180 |
| TTTTGCTCTA AGTCCTATGC TTCAGTCAGG GGCCAACCAA ATCTCACTGC CTCCTTTTTA | 240 |
| TCATGAAGCC TTTGATCACT GATAGTTCTT TTTATATCTT GAAAAATCAC CCTTCCCAGT | 300 |
| ACAGTTAATA TTTAGTATCT CTACTCATCT TGGCACTTAC TCACAGCTCC ATAATTCACT | 360 |
| CGTTTTTCGTA CCTCTTCATG GTGATGGGGA GCCCTTTGGA GGTGGTGA CTGCTTTATA | 420 |
| CTCCTCATGA TGCTTCACAT GTGGCAGGCG TGGAGTGCCC GGAGGCGGCC CTCCTGATTC | 480 |
| TGGGGCCTCC CAGG ATG GAG CCC CTG AGG CAC AGC CCA GGC CCT GGG GGG | 530 |
| Met Glu Pro Leu Arg His Ser Pro Gly Pro Gly Gly | |
| 1 5 10 | |
| CAA CGG CTA CTG CTG CCC TCC ATG CTG CTA GCA CTG CTG CTC CTG CTG | 578 |
| Gln Arg Leu Leu Leu Pro Ser Met Leu Leu Ala Leu Leu Leu Leu Leu | |
| 15 20 25 | |
| GCT CCA TCC CCA GGC CAC GCC ACT CGG GTA GTG TAC AAG GTG CCG GAG | 626 |
| Ala Pro Ser Pro Gly His Ala Thr Arg Val Val Tyr Lys Val Pro Glu | |
| 30 35 40 | |
| GAA CAG CCA CCC AAC ACC CTC ATT GGG AGC CTC GCA GCC GAC TAT GGT | 674 |
| Glu Gln Pro Pro Asn Thr Leu Ile Gly Ser Leu Ala Ala Asp Tyr Gly | |
| 45 50 55 60 | |
| TTT CCA GAT GTG GGG CAC CTG TAC AAG CTA GAG GTG GGT GCC CCG TAC | 722 |
| Phe Pro Asp Val Gly His Leu Tyr Lys Leu Glu Val Gly Ala Pro Tyr | |
| 65 70 75 | |
| CTT CGC GTG GAT GGC AAG ACA GGT GAC ATT TTC ACC ACC GAG ACC TCC | 770 |
| Leu Arg Val Asp Gly Lys Thr Gly Asp Ile Phe Thr Thr Glu Thr Ser | |
| 80 85 90 | |
| ATC GAC CGT GAG GGG CTC CGT GAA TGC CAG AAC CAG CTC CCT GGT GAT | 818 |
| Ile Asp Arg Glu Gly Leu Arg Glu Cys Gln Asn Gln Leu Pro Gly Asp | |
| 95 100 105 | |
| CCC TGC ATC CTG GAG TTT GAG GTA TCT ATC ACA GAC CTC GTG CAG AAT | 866 |
| Pro Cys Ile Leu Glu Phe Glu Val Ser Ile Thr Asp Leu Val Gln Asn | |
| 110 115 120 | |
| GCG AGC CCC CGG CTG CTA GAG GGC CAG ATA GAA GTA CAA GAC ATC AAT | 914 |
| Ala Ser Pro Arg Leu Leu Glu Gly Gln Ile Glu Val Gln Asp Ile Asn | |
| 125 130 135 140 | |
| GAC AAC ACA CCC AAC TTC GCC TCA CCA GTC ATC ACT CTG GCC ATC CCT | 962 |
| Asp Asn Thr Pro Asn Phe Ala Ser Pro Val Ile Thr Leu Ala Ile Pro | |
| 145 150 155 | |
| GAG AAC ACC AAC ATC GGC TCA CTC TTC CCC ATC CCG CTG GCT TCA GAC | 1010 |
| Glu Asn Thr Asn Ile Gly Ser Leu Phe Pro Ile Pro Leu Ala Ser Asp | |
| 160 165 170 | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| CGT | GAT | GCT | GGT | CCC | AAC | GGT | GTG | GCA | TCC | TAT | GAG | CTG | CAG | GTG | GCA | 1058 |
| Arg | Asp | Ala | Gly | Pro | Asn | Gly | Val | Ala | Ser | Tyr | Glu | Leu | Gln | Val | Ala | |
| | | 175 | | | | | 180 | | | | | 185 | | | | |
| GAG | GAC | CAG | GAG | GAG | AAG | CAA | CCA | CAG | CTC | ATT | GTG | ATG | GGC | AAC | CTG | 1106 |
| Glu | Asp | Gln | Glu | Glu | Lys | Gln | Pro | Gln | Leu | Ile | Val | Met | Gly | Asn | Leu | |
| | | 190 | | | | 195 | | | | | 200 | | | | | |
| GAC | CGT | GAG | CGC | TGG | GAC | TCC | TAT | GAC | CTC | ACC | ATC | AAG | GTG | CAG | GAT | 1154 |
| Asp | Arg | Glu | Arg | Trp | Asp | Ser | Tyr | Asp | Leu | Thr | Ile | Lys | Val | Gln | Asp | |
| 205 | | | | | 210 | | | | | 215 | | | | | 220 | |
| GGC | GGC | AGC | CCC | CCA | CGC | GCC | ACG | AGT | GCC | CTG | CTG | CGT | GTC | ACC | GTG | 1202 |
| Gly | Gly | Ser | Pro | Pro | Arg | Ala | Thr | Ser | Ala | Leu | Leu | Arg | Val | Thr | Val | |
| | | | | 225 | | | | | 230 | | | | | 235 | | |
| CTT | GAC | ACC | AAT | GAC | AAC | GCC | CCC | AAG | TTT | GAG | CGG | CCC | TCC | TAT | GAG | 1250 |
| Leu | Asp | Thr | Asn | Asp | Asn | Ala | Pro | Lys | Phe | Glu | Arg | Pro | Ser | Tyr | Glu | |
| | | | 240 | | | | | 245 | | | | | 250 | | | |
| GCC | GAA | CTA | TCT | GAG | AAT | AGC | CCC | ATA | GGC | CAC | TCG | GTC | ATC | CAG | GTG | 1298 |
| Ala | Glu | Leu | Ser | Glu | Asn | Ser | Pro | Ile | Gly | His | Ser | Val | Ile | Gln | Val | |
| | | 255 | | | | | 260 | | | | | 265 | | | | |
| AAG | GCC | AAT | GAC | TCA | GAC | CAA | GGT | GCC | AAT | GCA | GAA | ATC | GAA | TAC | ACA | 1346 |
| Lys | Ala | Asn | Asp | Ser | Asp | Gln | Gly | Ala | Asn | Ala | Glu | Ile | Glu | Tyr | Thr | |
| | | 270 | | | | 275 | | | | | 280 | | | | | |
| TTC | CAC | CAG | GCG | CCC | GAA | GTT | GTG | AGG | CGT | CTT | CTT | CGA | CTG | GAC | AGG | 1394 |
| Phe | His | Gln | Ala | Pro | Glu | Val | Val | Arg | Arg | Leu | Leu | Arg | Leu | Asp | Arg | |
| 285 | | | | | 290 | | | | | 295 | | | | | 300 | |
| AAC | ACT | GGA | CTT | ATC | ACT | GTT | CAG | GGC | CCG | GTG | GAC | CGT | GAG | GAC | CTA | 1442 |
| Asn | Thr | Gly | Leu | Ile | Thr | Val | Gln | Gly | Pro | Val | Asp | Arg | Glu | Asp | Leu | |
| | | | | 305 | | | | | 310 | | | | | 315 | | |
| AGC | ACC | CTG | CGC | TTC | TCA | GTG | CTT | GCT | AAG | GAC | CGA | GGC | ACC | AAC | CCC | 1490 |
| Ser | Thr | Leu | Arg | Phe | Ser | Val | Leu | Ala | Lys | Asp | Arg | Gly | Thr | Asn | Pro | |
| | | | 320 | | | | | 325 | | | | | 330 | | | |
| AAG | AGT | GCC | CGT | GCC | CAG | GTG | GTT | GTG | ACC | GTG | AAG | GAC | ATG | AAT | GAC | 1538 |
| Lys | Ser | Ala | Arg | Ala | Gln | Val | Val | Val | Thr | Val | Lys | Asp | Met | Asn | Asp | |
| | | 335 | | | | 340 | | | | | | 345 | | | | |
| AAT | GCC | CCC | ACC | ATT | GAG | ATC | CGG | GGC | ATA | GGG | CTA | GTG | ACT | CAT | CAA | 1586 |
| Asn | Ala | Pro | Thr | Ile | Glu | Ile | Arg | Gly | Ile | Gly | Leu | Val | Thr | His | Gln | |
| | | 350 | | | | 355 | | | | | 360 | | | | | |
| GAT | GGG | ATG | GCT | AAC | ATC | TCA | GAG | GAT | GTG | GCA | GAG | GAG | ACA | GCT | GTG | 1634 |
| Asp | Gly | Met | Ala | Asn | Ile | Ser | Glu | Asp | Val | Ala | Glu | Glu | Thr | Ala | Val | |
| 365 | | | | | 370 | | | | | 375 | | | | | 380 | |
| GCC | CTG | GTG | CAG | GTG | TCT | GAC | CGA | GAT | GAG | GGA | GAG | AAT | GCA | GCT | GTC | 1682 |
| Ala | Leu | Val | Gln | Val | Ser | Asp | Arg | Asp | Glu | Gly | Glu | Asn | Ala | Ala | Val | |
| | | | | 385 | | | | | 390 | | | | | 395 | | |
| ACC | TGT | GTG | GTG | GCA | GGT | GAT | GTG | CCC | TTC | CAG | CTG | CGC | CAG | GCC | AGT | 1730 |
| Thr | Cys | Val | Val | Ala | Gly | Asp | Val | Pro | Phe | Gln | Leu | Arg | Gln | Ala | Ser | |
| | | | 400 | | | | | 405 | | | | | 410 | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| GAG | ACA | GGC | AGT | GAC | AGC | AAG | AAG | AAG | TAT | TTC | CTG | CAG | ACT | ACC | ACC | 1778 |
| Glu | Thr | Gly | Ser | Asp | Ser | Lys | Lys | Lys | Tyr | Phe | Leu | Gln | Thr | Thr | Thr | |
| | | 415 | | | | | 420 | | | | | 425 | | | | |
| CCG | CTA | GAC | TAC | GAG | AAG | GTC | AAA | GAC | TAC | ACC | ATT | GAG | ATT | GTG | GCT | 1826 |
| Pro | Leu | Asp | Tyr | Glu | Lys | Val | Lys | Asp | Tyr | Thr | Ile | Glu | Ile | Val | Ala | |
| | 430 | | | | | 435 | | | | | 440 | | | | | |
| GTG | GAC | TCT | GGC | AAC | CCC | CCA | CTC | TCC | AGC | ACT | AAC | TCC | CTC | AAG | GTG | 1874 |
| Val | Asp | Ser | Gly | Asn | Pro | Pro | Leu | Ser | Ser | Thr | Asn | Ser | Leu | Lys | Val | |
| | 445 | | | | 450 | | | | | 455 | | | | | 460 | |
| CAG | GTG | GTG | GAC | GTC | AAT | GAC | AAC | GCA | CCT | GTC | TTC | ACT | CAG | AGT | GTC | 1922 |
| Gln | Val | Val | Asp | Val | Asn | Asp | Asn | Ala | Pro | Val | Phe | Thr | Gln | Ser | Val | |
| | | | | 465 | | | | | 470 | | | | | 475 | | |
| ACT | GAG | GTC | GCC | TTC | CCG | GAA | AAC | AAC | AAG | CCT | GGT | GAA | GTG | ATT | GCT | 1970 |
| Thr | Glu | Val | Ala | Phe | Pro | Glu | Asn | Asn | Lys | Pro | Gly | Glu | Val | Ile | Ala | |
| | | | 480 | | | | | 485 | | | | | 490 | | | |
| GAG | ATC | ACT | GCC | AGT | GAT | GCT | GAC | TCT | GGC | TCT | AAT | GCT | GAG | CTG | GTT | 2018 |
| Glu | Ile | Thr | Ala | Ser | Asp | Ala | Asp | Ser | Gly | Ser | Asn | Ala | Glu | Leu | Val | |
| | | 495 | | | | | 500 | | | | | 505 | | | | |
| TAC | TCT | CTG | GAG | CCT | GAG | CCG | GCT | GCT | AAG | GGC | CTC | TTC | ACC | ATC | TCA | 2066 |
| Tyr | Ser | Leu | Glu | Pro | Glu | Pro | Ala | Ala | Lys | Gly | Leu | Phe | Thr | Ile | Ser | |
| | 510 | | | | | 515 | | | | | 520 | | | | | |
| CCC | GAG | ACT | GGA | GAG | ATC | CAG | GTG | AAG | ACA | TCT | CTG | GAT | CGG | GAA | CAG | 2114 |
| Pro | Glu | Thr | Gly | Glu | Ile | Gln | Val | Lys | Thr | Ser | Leu | Asp | Arg | Glu | Gln | |
| | 525 | | | | 530 | | | | | 535 | | | | | 540 | |
| CGG | GAG | AGC | TAT | GAG | TTG | AAG | GTG | GTG | GCA | GCT | GAC | CGG | GGC | AGT | CCT | 2162 |
| Arg | Glu | Ser | Tyr | Glu | Leu | Lys | Val | Val | Ala | Ala | Asp | Arg | Gly | Ser | Pro | |
| | | | | 545 | | | | | 550 | | | | | 555 | | |
| AGC | CTC | CAG | GGC | ACA | GCC | ACT | GTC | CTT | GTC | AAT | GTG | CTG | GAC | TGC | AAT | 2210 |
| Ser | Leu | Gln | Gly | Thr | Ala | Thr | Val | Leu | Val | Asn | Val | Leu | Asp | Cys | Asn | |
| | | | 560 | | | | 565 | | | | | | 570 | | | |
| GAC | AAT | GAC | CCC | AAA | TTT | ATG | CTG | AGT | GGC | TAC | AAC | TTC | TCA | GTG | ATG | 2258 |
| Asp | Asn | Asp | Pro | Lys | Phe | Met | Leu | Ser | Gly | Tyr | Asn | Phe | Ser | Val | Met | |
| | | 575 | | | | | 580 | | | | | 585 | | | | |
| GAG | AAC | ATG | CCA | GCA | CTG | AGT | CCA | GTG | GGC | ATG | GTG | ACT | GTG | ATT | GAT | 2306 |
| Glu | Asn | Met | Pro | Ala | Leu | Ser | Pro | Val | Gly | Met | Val | Thr | Val | Ile | Asp | |
| | 590 | | | | | 595 | | | | | 600 | | | | | |
| GGA | GAC | AAG | GGG | GAG | AAT | GCC | CAG | GTG | CAG | CTC | TCA | GTG | GAG | CAG | GAC | 2354 |
| Gly | Asp | Lys | Gly | Glu | Asn | Ala | Gln | Val | Gln | Leu | Ser | Val | Glu | Gln | Asp | |
| | 605 | | | | 610 | | | | | 615 | | | | | 620 | |
| AAC | GGT | GAC | TTT | GTT | ATC | CAG | AAT | GGC | ACA | GGC | ACC | ATC | CTA | TCC | AGC | 2402 |
| Asn | Gly | Asp | Phe | Val | Ile | Gln | Asn | Gly | Thr | Gly | Thr | Ile | Leu | Ser | Ser | |
| | | | | 625 | | | | | 630 | | | | | 635 | | |
| CTG | AGC | TTT | GAT | CGA | GAG | CAA | CAA | AGC | ACC | TAC | ACC | TTC | CAG | CTG | AAG | 2450 |
| Leu | Ser | Phe | Asp | Arg | Glu | Gln | Gln | Ser | Thr | Tyr | Thr | Phe | Gln | Leu | Lys | |
| | | | 640 | | | | | 645 | | | | | 650 | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| GCA | GTG | GAT | GGT | GGC | GTC | CCA | CCT | CGC | TCA | GCT | TAC | GTT | GGT | GTC | ACC | 2498 |
| Ala | Val | Asp | Gly | Gly | Val | Pro | Pro | Arg | Ser | Ala | Tyr | Val | Gly | Val | Thr | |
| | 655 | | | | | | 660 | | | | | 665 | | | | |
| ATC | AAT | GTG | CTG | GAC | GAG | AAT | GAC | AAC | GCA | CCC | TAT | ATC | ACT | GCC | CCT | 2546 |
| Ile | Asn | Val | Leu | Asp | Glu | Asn | Asp | Asn | Ala | Pro | Tyr | Ile | Thr | Ala | Pro | |
| | 670 | | | | | 675 | | | | | 680 | | | | | |
| TCT | AAC | ACC | TCT | CAC | AAG | CTG | CTG | ACC | CCC | CAG | ACA | CGT | CTT | GGT | GAG | 2594 |
| Ser | Asn | Thr | Ser | His | Lys | Leu | Leu | Thr | Pro | Gln | Thr | Arg | Leu | Gly | Glu | |
| | 685 | | | | 690 | | | | | 695 | | | | | 700 | |
| ACG | GTC | AGC | CAG | GTG | GCA | GCC | GAG | GAC | TTT | GAC | TCT | GGT | GTC | AAT | GCC | 2642 |
| Thr | Val | Ser | Gln | Val | Ala | Ala | Glu | Asp | Phe | Asp | Ser | Gly | Val | Asn | Ala | |
| | | | | 705 | | | | | 710 | | | | | 715 | | |
| GAG | CTG | ATC | TAC | AGC | ATT | GCA | GGT | GGC | AAC | CCT | TAT | GGA | CTC | TTC | CAG | 2690 |
| Glu | Leu | Ile | Tyr | Ser | Ile | Ala | Gly | Gly | Asn | Pro | Tyr | Gly | Leu | Phe | Gln | |
| | | | 720 | | | | | 725 | | | | | 730 | | | |
| ATT | GGG | TCA | CAT | TCA | GGT | GCC | ATC | ACC | CTG | GAG | AAG | GAG | ATT | GAG | CGG | 2738 |
| Ile | Gly | Ser | His | Ser | Gly | Ala | Ile | Thr | Leu | Glu | Lys | Glu | Ile | Glu | Arg | |
| | 735 | | | | | | 740 | | | | | 745 | | | | |
| CGC | CAC | CAT | GGG | CTA | CAC | CGC | CTG | GTG | GTG | AAG | GTC | AGT | GAC | CGC | GGC | 2786 |
| Arg | His | His | Gly | Leu | His | Arg | Leu | Val | Val | Lys | Val | Ser | Asp | Arg | Gly | |
| | 750 | | | | | 755 | | | | | 760 | | | | | |
| AAG | CCC | CCA | CGC | TAT | GGC | ACA | GCC | TTG | GTC | CAT | CTT | TAT | GTC | AAT | GAG | 2834 |
| Lys | Pro | Pro | Arg | Tyr | Gly | Thr | Ala | Leu | Val | His | Leu | Tyr | Val | Asn | Glu | |
| | 765 | | | | 770 | | | | | 775 | | | | | 780 | |
| ACT | CTG | GCC | AAC | CGC | ACG | CTG | CTG | GAG | ACC | CTC | CTG | GGC | CAC | AGC | CTG | 2882 |
| Thr | Leu | Ala | Asn | Arg | Thr | Leu | Leu | Glu | Thr | Leu | Leu | Gly | His | Ser | Leu | |
| | | | | 785 | | | | | 790 | | | | | 795 | | |
| GAC | ACG | CCG | CTG | GAT | ATT | GAC | ATT | GCT | GGG | GAT | CCA | GAA | TAT | GAG | CGC | 2930 |
| Asp | Thr | Pro | Leu | Asp | Ile | Asp | Ile | Ala | Gly | Asp | Pro | Glu | Tyr | Glu | Arg | |
| | | | 800 | | | | | 805 | | | | | 810 | | | |
| TCC | AAG | CAG | CGT | GGC | AAC | ATT | CTC | TTT | GGT | GTG | GTG | GCT | GGT | GTG | GTG | 2978 |
| Ser | Lys | Gln | Arg | Gly | Asn | Ile | Leu | Phe | Gly | Val | Val | Ala | Gly | Val | Val | |
| | 815 | | | | | | 820 | | | | | 825 | | | | |
| GCC | GTG | GCC | TTG | CTC | ATC | GCC | CTG | GCG | GTT | CTT | GTG | CGC | TAC | TGC | AGA | 3026 |
| Ala | Val | Ala | Leu | Leu | Ile | Ala | Leu | Ala | Val | Leu | Val | Arg | Tyr | Cys | Arg | |
| | 830 | | | | | 835 | | | | | 840 | | | | | |
| CAG | CGG | GAG | GCC | AAA | AGT | GGT | TAC | CAG | GCT | GGT | AAG | AAG | GAG | ACC | AAG | 3074 |
| Gln | Arg | Glu | Ala | Lys | Ser | Gly | Tyr | Gln | Ala | Gly | Lys | Lys | Glu | Thr | Lys | |
| | 845 | | | | 850 | | | | | 855 | | | | | 860 | |
| GAC | CTG | TAT | GCC | CCC | AAG | CCC | AGT | GGC | AAG | GCC | TCC | AAG | GGA | AAC | AAA | 3122 |
| Asp | Leu | Tyr | Ala | Pro | Lys | Pro | Ser | Gly | Lys | Ala | Ser | Lys | Gly | Asn | Lys | |
| | | | | 865 | | | | | 870 | | | | | 875 | | |
| AGC | AAA | GGC | AAG | AAG | AGC | AAG | TCC | CCA | AAG | CCC | GTG | AAG | CCA | GTG | GAG | 3170 |
| Ser | Lys | Gly | Lys | Lys | Ser | Lys | Ser | Pro | Lys | Pro | Val | Lys | Pro | Val | Glu | |
| | | | 880 | | | | | 885 | | | | | 890 | | | |

| | | | | | | | | | | | | | | | | |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------|
| GAC Asp | GAG Glu | GAT Asp | GAG Glu | GCC Ala | GGG Gly | CTG Leu | CAG Gln | AAG Lys | TCC Ser | CTC Leu | AAG Lys | TTC Phe | AAC Asn | CTG Leu | ATG Met | 3218 |
| | 895 | | | | | | 900 | | | | | 905 | | | | |
| AGC Ser | GAT Asp | GCC Ala | CCT Pro | GGG Gly | GAC Asp | AGT Ser | CCC Pro | CGC Arg | ATC Ile | CAC His | CTG Leu | CCC Pro | CTC Leu | AAC Asn | TAC Tyr | 3266 |
| | 910 | | | | | 915 | | | | | 920 | | | | | |
| CCA Pro | CCA Pro | GGC Gly | AGC Ser | CCT Pro | GAC Asp | CTG Leu | GGC Gly | CGC Arg | CAC His | TAT Tyr | CGC Arg | TCT Ser | AAC Asn | TCC Ser | CCA Pro | 3314 |
| | 925 | | | | 930 | | | | | 935 | | | | | 940 | |
| CTG Leu | CCT Pro | TCC Ser | ATC Ile | CAG Gln | CTG Leu | CAG Gln | CCC Pro | CAG Gln | TCA Ser | CCC Pro | TCA Ser | GCC Ala | TCC Ser | AAG Lys | AAG Lys | 3362 |
| | | | | 945 | | | | | 950 | | | | | 955 | | |
| CAC His | CAG Gln | GTG Val | GTA Val | CAG Gln | GAC Asp | CTG Leu | CCA Pro | CCT Pro | GCA Ala | AAC Asn | ACA Thr | TTC Phe | GTG Val | GGC Gly | ACC Thr | 3410 |
| | | | 960 | | | | | 965 | | | | | 970 | | | |
| GGG Gly | GAC Asp | ACC Thr | ACG Thr | TCC Ser | ACG Thr | GGC Gly | TCT Ser | GAG Glu | CAG Gln | TAC Tyr | TCC Ser | GAC Asp | TAC Tyr | AGC Ser | TAC Tyr | 3458 |
| | | 975 | | | | | 980 | | | | | 985 | | | | |
| CGC Arg | ACC Thr | AAC Asn | CCC Pro | CCC Pro | AAA Lys | TAC Tyr | CCC Pro | AGC Ser | AAG Lys | CAG Gln | TTA Leu | CCT Pro | CAC His | CGC Arg | CGC Arg | 3506 |
| | 990 | | | | | 995 | | | | | 1000 | | | | | |
| GTC Val | ACC Thr | TTC Phe | TCG Ser | GCC Ala | ACC Thr | AGC Ser | CAG Gln | GCC Ala | CAG Gln | GAG Glu | CTG Leu | CAG Gln | GAC Asp | CCA Pro | TCC Ser | 3554 |
| | 1005 | | | | 1010 | | | | | 1015 | | | | | 1020 | |
| CAG Gln | CAC His | AGT Ser | TAC Tyr | TAT Tyr | GAC Asp | AGT Ser | GGC Gly | CTG Leu | GAG Glu | GAG Glu | TCT Ser | GAG Glu | ACG Thr | CCG Pro | TCC Ser | 3602 |
| | | | | 1025 | | | | | 1030 | | | | | 1035 | | |
| AGC Ser | AAG Lys | TCA Ser | TCC Ser | TCA Ser | GGG Gly | CCT Pro | CGA Arg | CTC Leu | GGT Gly | CCC Pro | CTG Leu | GCC Ala | CTG Leu | CCT Pro | GAG Glu | 3650 |
| | | | 1040 | | | | | 1045 | | | | | 1050 | | | |
| GAT Asp | CAC His | TAT Tyr | GAG Glu | CGC Arg | ACC Thr | ACC Thr | CCT Pro | GAT Asp | GGC Gly | AGC Ser | ATA Ile | GGA Gly | GAG Glu | ATG Met | GAG Glu | 3698 |
| | | 1055 | | | | | 1060 | | | | | 1065 | | | | |
| CAC His | CCC Pro | GAG Glu | AAT Asn | GAC Asp | CTT Leu | CGC Arg | CCT Pro | TTG Leu | CCT Pro | GAT Asp | GTC Val | GCC Ala | ATG Met | ACA Thr | GGC Gly | 3746 |
| | 1070 | | | | | 1075 | | | | | 1080 | | | | | |
| ACA Thr | TGT Cys | ACC Thr | CGG Arg | GAG Glu | TGC Cys | AGT Ser | GAG Glu | TTT Phe | GGC Gly | CAC His | TCT Ser | GAC Asp | ACA Thr | TGC Cys | TGG Trp | 3794 |
| | 1085 | | | | 1090 | | | | | 1095 | | | | | 1100 | |
| ATG Met | CCT Pro | GGC Gly | CAG Gln | TCA Ser | TCT Ser | CCC Pro | AGC Ser | CGC Arg | CGG Arg | ACC Thr | AAG Lys | AGC Ser | AGC Ser | GCC Ala | CTC Leu | 3842 |
| | | | | 1105 | | | | | 1110 | | | | | 1115 | | |
| AAA Lys | CTC Leu | TCC Ser | ACC Thr | TTC Phe | ATG Met | CCT Pro | TAC Tyr | CAG Gln | GAC Asp | CGA Arg | GGA Gly | GGG Gly | CAG Gln | GAG Glu | CCT Pro | 3890 |
| | | | 1120 | | | | | 1125 | | | | | 1130 | | | |
| GCG Ala | GGC Gly | GCC Ala | GGC Gly | AGC Ser | CCC Pro | AGC Ser | CCC Pro | CCG Pro | GAA Glu | GAC Asp | CGG Arg | AAC Asn | ACC Thr | AAA Lys | ACG Thr | 3938 |

| 1135 | 1140 | 1145 | |
|---|------|------|------|
| GCC CCC GTG CGC CTC CTG CCC TCC TAC AGT GCC TTC TCC CAC AGT AGC | | | 3986 |
| Ala Pro Val Arg Leu Leu Pro Ser Tyr Ser Ala Phe Ser His Ser Ser | | | |
| 1150 | 1155 | 1160 | |
| CAT GAT TCC TGC AAG GAC TCG GCC ACC TTG GAG GAA ATC CCC CTG ACC | | | 4034 |
| His Asp Ser Cys Lys Asp Ser Ala Thr Leu Glu Glu Ile Pro Leu Thr | | | |
| 1165 | 1170 | 1175 | 1180 |
| CAG ACC TCG GAC TTC CCA CCC GCA GCC ACA CCG GCA TCT GCC CAG ACG | | | 4082 |
| Gln Thr Ser Asp Phe Pro Pro Ala Ala Thr Pro Ala Ser Ala Gln Thr | | | |
| | 1185 | 1190 | 1195 |
| GCC AAG CGC GAG ATC TAC CTG TGAGCCCCCT ACTGGCCGGC CCCCCTCCCC | | | 4133 |
| Ala Lys Arg Glu Ile Tyr Leu | | | |
| 1200 | | | |
| CAGCGCCGGC CAGCTCCCAA ATGCCCATTC CAGGGCCTCA CTCTCCACCC CTTCAGCGTG | | | 4193 |
| GACTTCCTGC CAGGGCCCAA GTGGGGGTAT CACTGACCTC ATGACCACGC TGGCCCTTCT | | | 4253 |
| CCCATGCAGG GTCCAGGTCC TCTCCCCTCA TTTCCATCTC CCAGCCCAGG GGCCCCTTCC | | | 4313 |
| CCTTTATGGG GCTTCCCCCA GCTGATGCCC AAGAGGGCTC CTCTGCAATG ACTGGGCTCC | | | 4373 |
| TTCCCTTGAC TTCCAGGGAG CACCCCCTCG ATTTGGGCAG ATGGTGGAGT CAAGGGTGGG | | | 4433 |
| CAGCGTACTT CTAACTCATT GTTTCCCTCA TGGCCGACCA GGGCGGGGAT AGCATGCCCA | | | 4493 |
| ATTTTAGCCC TGAAGCAGGG CTGAACTGGG GAGCCCCTTT CCCTGGGAGC TCCCAGAGGA | | | 4553 |
| AACTCTTGAC CACCAGTGGC TCCCTGAAGG GCTTTTGTTA CCAAAGGTGG GGTAGGGACG | | | 4613 |
| GGGGTGGGAG TGGAGCGGAG GCCTTGTTTT CCCGTGG | | | 4650 |

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1203 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Pro | Leu | Arg | His | Ser | Pro | Gly | Pro | Gly | Gly | Gln | Arg | Leu | Leu |
| 1 | | | | | 5 | | | | 10 | | | | | 15 | |
| Leu | Pro | Ser | Met | Leu | Leu | Ala | Leu | Leu | Leu | Leu | Ala | Pro | Ser | Pro | |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Gly | His | Ala | Thr | Arg | Val | Val | Tyr | Lys | Val | Pro | Glu | Glu | Gln | Pro | Pro |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Asn | Thr | Leu | Ile | Gly | Ser | Leu | Ala | Ala | Asp | Tyr | Gly | Phe | Pro | Asp | Val |
| | | 50 | | | | 55 | | | | | | 60 | | | |

Gly His Leu Tyr Lys Leu Glu Val Gly Ala Pro Tyr Leu Arg Val Asp
 65 70 75 80
 Gly Lys Thr Gly Asp Ile Phe Thr Thr Glu Thr Ser Ile Asp Arg Glu
 85 90 95
 Gly Leu Arg Glu Cys Gln Asn Gln Leu Pro Gly Asp Pro Cys Ile Leu
 100 105 110
 Glu Phe Glu Val Ser Ile Thr Asp Leu Val Gln Asn Ala Ser Pro Arg
 115 120 125
 Leu Leu Glu Gly Gln Ile Glu Val Gln Asp Ile Asn Asp Asn Thr Pro
 130 135 140
 Asn Phe Ala Ser Pro Val Ile Thr Leu Ala Ile Pro Glu Asn Thr Asn
 145 150 155 160
 Ile Gly Ser Leu Phe Pro Ile Pro Leu Ala Ser Asp Arg Asp Ala Gly
 165 170 175
 Pro Asn Gly Val Ala Ser Tyr Glu Leu Gln Val Ala Glu Asp Gln Glu
 180 185 190
 Glu Lys Gln Pro Gln Leu Ile Val Met Gly Asn Leu Asp Arg Glu Arg
 195 200 205
 Trp Asp Ser Tyr Asp Leu Thr Ile Lys Val Gln Asp Gly Gly Ser Pro
 210 215 220
 Pro Arg Ala Thr Ser Ala Leu Leu Arg Val Thr Val Leu Asp Thr Asn
 225 230 235 240
 Asp Asn Ala Pro Lys Phe Glu Arg Pro Ser Tyr Glu Ala Glu Leu Ser
 245 250 255
 Glu Asn Ser Pro Ile Gly His Ser Val Ile Gln Val Lys Ala Asn Asp
 260 265 270
 Ser Asp Gln Gly Ala Asn Ala Glu Ile Glu Tyr Thr Phe His Gln Ala
 275 280 285
 Pro Glu Val Val Arg Arg Leu Leu Arg Leu Asp Arg Asn Thr Gly Leu
 290 295 300
 Ile Thr Val Gln Gly Pro Val Asp Arg Glu Asp Leu Ser Thr Leu Arg
 305 310 315 320
 Phe Ser Val Leu Ala Lys Asp Arg Gly Thr Asn Pro Lys Ser Ala Arg
 325 330 335
 Ala Gln Val Val Val Thr Val Lys Asp Met Asn Asp Asn Ala Pro Thr
 340 345 350
 Ile Glu Ile Arg Gly Ile Gly Leu Val Thr His Gln Asp Gly Met Ala
 355 360 365
 Asn Ile Ser Glu Asp Val Ala Glu Glu Thr Ala Val Ala Leu Val Gln
 370 375 380
 Val Ser Asp Arg Asp Glu Gly Glu Asn Ala Ala Val Thr Cys Val Val
 385 390 395 400

Ala Gly Asp Val Pro Phe Gln Leu Arg Gln Ala Ser Glu Thr Gly Ser
405 410 415

Asp Ser Lys Lys Lys Tyr Phe Leu Gln Thr Thr Thr Pro Leu Asp Tyr
420 425 430

Glu Lys Val Lys Asp Tyr Thr Ile Glu Ile Val Ala Val Asp Ser Gly
435 440 445

Asn Pro Pro Leu Ser Ser Thr Asn Ser Leu Lys Val Gln Val Val Asp
450 455 460

Val Asn Asp Asn Ala Pro Val Phe Thr Gln Ser Val Thr Glu Val Ala
465 470 475 480

Phe Pro Glu Asn Asn Lys Pro Gly Glu Val Ile Ala Glu Ile Thr Ala
485 490 495

Ser Asp Ala Asp Ser Gly Ser Asn Ala Glu Leu Val Tyr Ser Leu Glu
500 505 510

Pro Glu Pro Ala Ala Lys Gly Leu Phe Thr Ile Ser Pro Glu Thr Gly
515 520 525

Glu Ile Gln Val Lys Thr Ser Leu Asp Arg Glu Gln Arg Glu Ser Tyr
530 535 540

Glu Leu Lys Val Val Ala Ala Asp Arg Gly Ser Pro Ser Leu Gln Gly
545 550 555 560

Thr Ala Thr Val Leu Val Asn Val Leu Asp Cys Asn Asp Asn Asp Pro
565 570 575

Lys Phe Met Leu Ser Gly Tyr Asn Phe Ser Val Met Glu Asn Met Pro
580 585 590

Ala Leu Ser Pro Val Gly Met Val Thr Val Ile Asp Gly Asp Lys Gly
595 600 605

Glu Asn Ala Gln Val Gln Leu Ser Val Glu Gln Asp Asn Gly Asp Phe
610 615 620

Val Ile Gln Asn Gly Thr Gly Thr Ile Leu Ser Ser Leu Ser Phe Asp
625 630 635 640

Arg Glu Gln Gln Ser Thr Tyr Thr Phe Gln Leu Lys Ala Val Asp Gly
645 650 655

Gly Val Pro Pro Arg Ser Ala Tyr Val Gly Val Thr Ile Asn Val Leu
660 665 670

Asp Glu Asn Asp Asn Ala Pro Tyr Ile Thr Ala Pro Ser Asn Thr Ser
675 680 685

His Lys Leu Leu Thr Pro Gln Thr Arg Leu Gly Glu Thr Val Ser Gln
690 695 700

Val Ala Ala Glu Asp Phe Asp Ser Gly Val Asn Ala Glu Leu Ile Tyr
705 710 715 720

Ser Ile Ala Gly Gly Asn Pro Tyr Gly Leu Phe Gln Ile Gly Ser His
725 730 735

| | | | | | | | | | | | | | | | | |
|------|------|-----|------|------|------|------|------|------|------|------|------|------|-----|------|------|--|
| Ser | Gly | Ala | Ile | Thr | Leu | Glu | Lys | Glu | Ile | Glu | Arg | Arg | His | His | Gly | |
| | | | 740 | | | | | 745 | | | | | 750 | | | |
| Leu | His | Arg | Leu | Val | Val | Lys | Val | Ser | Asp | Arg | Gly | Lys | Pro | Pro | Arg | |
| | | 755 | | | | | 760 | | | | | 765 | | | | |
| Tyr | Gly | Thr | Ala | Leu | Val | His | Leu | Tyr | Val | Asn | Glu | Thr | Leu | Ala | Asn | |
| | 770 | | | | | 775 | | | | | 780 | | | | | |
| Arg | Thr | Leu | Leu | Glu | Thr | Leu | Leu | Gly | His | Ser | Leu | Asp | Thr | Pro | Leu | |
| 785 | | | | | 790 | | | | | 795 | | | | | 800 | |
| Asp | Ile | Asp | Ile | Ala | Gly | Asp | Pro | Glu | Tyr | Glu | Arg | Ser | Lys | Gln | Arg | |
| | | | | 805 | | | | | 810 | | | | | 815 | | |
| Gly | Asn | Ile | Leu | Phe | Gly | Val | Val | Ala | Gly | Val | Val | Ala | Val | Ala | Leu | |
| | | 820 | | | | | | 825 | | | | | 830 | | | |
| Leu | Ile | Ala | Leu | Ala | Val | Leu | Val | Arg | Tyr | Cys | Arg | Gln | Arg | Glu | Ala | |
| | | 835 | | | | | 840 | | | | | 845 | | | | |
| Lys | Ser | Gly | Tyr | Gln | Ala | Gly | Lys | Lys | Glu | Thr | Lys | Asp | Leu | Tyr | Ala | |
| | 850 | | | | | 855 | | | | | 860 | | | | | |
| Pro | Lys | Pro | Ser | Gly | Lys | Ala | Ser | Lys | Gly | Asn | Lys | Ser | Lys | Gly | Lys | |
| 865 | | | | | 870 | | | | | 875 | | | | | 880 | |
| Lys | Ser | Lys | Ser | Pro | Lys | Pro | Val | Lys | Pro | Val | Glu | Asp | Glu | Asp | Glu | |
| | | | | 885 | | | | | 890 | | | | | 895 | | |
| Ala | Gly | Leu | Gln | Lys | Ser | Leu | Lys | Phe | Asn | Leu | Met | Ser | Asp | Ala | Pro | |
| | | | 900 | | | | | 905 | | | | | 910 | | | |
| Gly | Asp | Ser | Pro | Arg | Ile | His | Leu | Pro | Leu | Asn | Tyr | Pro | Pro | Gly | Ser | |
| | | 915 | | | | | 920 | | | | | 925 | | | | |
| Pro | Asp | Leu | Gly | Arg | His | Tyr | Arg | Ser | Asn | Ser | Pro | Leu | Pro | Ser | Ile | |
| | 930 | | | | | 935 | | | | | 940 | | | | | |
| Gln | Leu | Gln | Pro | Gln | Ser | Pro | Ser | Ala | Ser | Lys | Lys | His | Gln | Val | Val | |
| 945 | | | | | 950 | | | | | 955 | | | | | 960 | |
| Gln | Asp | Leu | Pro | Pro | Ala | Asn | Thr | Phe | Val | Gly | Thr | Gly | Asp | Thr | Thr | |
| | | | | 965 | | | | | 970 | | | | | 975 | | |
| Ser | Thr | Gly | Ser | Glu | Gln | Tyr | Ser | Asp | Tyr | Ser | Tyr | Arg | Thr | Asn | Pro | |
| | | | 980 | | | | | 985 | | | | | 990 | | | |
| Pro | Lys | Tyr | Pro | Ser | Lys | Gln | Leu | Pro | His | Arg | Arg | Val | Thr | Phe | Ser | |
| | | 995 | | | | | 1000 | | | | | 1005 | | | | |
| Ala | Thr | Ser | Gln | Ala | Gln | Glu | Leu | Gln | Asp | Pro | Ser | Gln | His | Ser | Tyr | |
| | 1010 | | | | | 1015 | | | | | 1020 | | | | | |
| Tyr | Asp | Ser | Gly | Leu | Glu | Glu | Ser | Glu | Thr | Pro | Ser | Ser | Lys | Ser | Ser | |
| 1025 | | | | | 1030 | | | | | 1035 | | | | | 1040 | |
| Ser | Gly | Pro | Arg | Leu | Gly | Pro | Leu | Ala | Leu | Pro | Glu | Asp | His | Tyr | Glu | |
| | | | | 1045 | | | | | 1050 | | | | | 1055 | | |
| Arg | Thr | Thr | Pro | Asp | Gly | Ser | Ile | Gly | Glu | Met | Glu | His | Pro | Glu | Asn | |
| | | | 1060 | | | | | 1065 | | | | | | 1070 | | |

Asp Leu Arg Pro Leu Pro Asp Val Ala Met Thr Gly Thr Cys Thr Arg
 1075 1080 1085

Glu Cys Ser Glu Phe Gly His Ser Asp Thr Cys Trp Met Pro Gly Gln
 1090 1095 1100

Ser Ser Pro Ser Arg Arg Thr Lys Ser Ser Ala Leu Lys Leu Ser Thr
 1105 1110 1115 1120

Phe Met Pro Tyr Gln Asp Arg Gly Gly Gln Glu Pro Ala Gly Ala Gly
 1125 1130 1135

Ser Pro Ser Pro Pro Glu Asp Arg Asn Thr Lys Thr Ala Pro Val Arg
 1140 1145 1150

Leu Leu Pro Ser Tyr Ser Ala Phe Ser His Ser Ser His Asp Ser Cys
 1155 1160 1165

Lys Asp Ser Ala Thr Leu Glu Glu Ile Pro Leu Thr Gln Thr Ser Asp
 1170 1175 1180

Phe Pro Pro Ala Ala Thr Pro Ala Ser Ala Gln Thr Ala Lys Arg Glu
 1185 1190 1195 1200

Ile Tyr Leu

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2789 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 115..2622

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

| | |
|---|-----|
| CGAAAGCCAT GTCGGACTCG TCGCCAGCG CCAAGCGCT AACCCGCTGA AAGTTTCTCA | 60 |
| GCGAAATCTC AGGGACGATC TGGACCCCGC TGAGAGGAAC TGCTTTTGAG TGAG ATG | 117 |
| | Met |
| | 1 |
| GTC CCA GAG GCC TGG AGG AGC GGA CTG GTA AGC ACC GGG AGG GTA GTG | 165 |
| Val Pro Glu Ala Trp Arg Ser Gly Leu Val Ser Thr Gly Arg Val Val | |
| 5 10 15 | |
| GGA GTT TTG CTT CTG CTT GGT GCC TTG AAC AAG GCT TCC ACG GTC ATT | 213 |
| Gly Val Leu Leu Leu Leu Gly Ala Leu Asn Lys Ala Ser Thr Val Ile | |
| 20 25 30 | |
| CAC TAT GAG ATC CCG GAG GAA AGA GAG AAG GGT TTC GCT GTG GGC AAC | 261 |
| His Tyr Glu Ile Pro Glu Glu Arg Glu Lys Gly Phe Ala Val Gly Asn | |
| 35 40 45 | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| GTG | GTC | GCG | AAC | CTT | GGT | TTG | GAT | CTC | GGT | AGC | CTC | TCA | GCC | CGC | AGG | 309 |
| Val | Val | Ala | Asn | Leu | Gly | Leu | Asp | Leu | Gly | Ser | Leu | Ser | Ala | Arg | Arg | |
| 50 | | | | | 55 | | | | | 60 | | | | | 65 | |
| TTC | CCG | GTG | GTG | TCT | GGA | GCT | AGC | CGA | AGA | TTC | TTT | GAG | GTG | AAC | CGG | 357 |
| Phe | Pro | Val | Val | Ser | Gly | Ala | Ser | Arg | Arg | Phe | Phe | Glu | Val | Asn | Arg | |
| | | | | 70 | | | | | 75 | | | | | 80 | | |
| GAG | ACC | GGA | GAG | ATG | TTT | GTG | AAC | GAC | CGT | CTG | GAT | CGA | GAG | GAG | CTG | 405 |
| Glu | Thr | Gly | Glu | Met | Phe | Val | Asn | Asp | Arg | Leu | Asp | Arg | Glu | Glu | Leu | |
| | | | 85 | | | | | 90 | | | | | 95 | | | |
| TGT | GGG | ACA | CTG | CCC | TCT | TGC | ACT | GTA | ACT | CTG | GAG | TTG | GTA | GTG | GAG | 453 |
| Cys | Gly | Thr | Leu | Pro | Ser | Cys | Thr | Val | Thr | Leu | Glu | Leu | Val | Val | Glu | |
| | | 100 | | | | | 105 | | | | | 110 | | | | |
| AAC | CCG | CTG | GAG | CTG | TTC | AGC | GTG | GAA | GTG | GTG | ATC | CAG | GAC | ATC | AAC | 501 |
| Asn | Pro | Leu | Glu | Leu | Phe | Ser | Val | Glu | Val | Val | Ile | Gln | Asp | Ile | Asn | |
| | 115 | | | | | 120 | | | | | 125 | | | | | |
| GAC | AAC | AAT | CCT | GCT | TTC | CCT | ACC | CAG | GAA | ATG | AAA | TTG | GAG | ATT | AGC | 549 |
| Asp | Asn | Asn | Pro | Ala | Phe | Pro | Thr | Gln | Glu | Met | Lys | Leu | Glu | Ile | Ser | |
| 130 | | | | | 135 | | | | | 140 | | | | | 145 | |
| GAG | GCC | GTG | GCT | CCG | GGG | ACG | CGC | TTT | CCG | CTC | GAG | AGC | GCG | CAC | GAT | 597 |
| Glu | Ala | Val | Ala | Pro | Gly | Thr | Arg | Phe | Pro | Leu | Glu | Ser | Ala | His | Asp | |
| | | | | 150 | | | | | 155 | | | | | 160 | | |
| CCC | GAT | CTG | GGA | AGC | AAC | TCT | TTA | CAA | ACC | TAT | GAG | CTG | AGC | CGA | AAT | 645 |
| Pro | Asp | Leu | Gly | Ser | Asn | Ser | Leu | Gln | Thr | Tyr | Glu | Leu | Ser | Arg | Asn | |
| | | | 165 | | | | | 170 | | | | | 175 | | | |
| GAA | TAC | TTT | GCG | CTT | CGC | GTG | CAG | ACG | CGG | GAG | GAC | AGC | ACC | AAG | TAC | 693 |
| Glu | Tyr | Phe | Ala | Leu | Arg | Val | Gln | Thr | Arg | Glu | Asp | Ser | Thr | Lys | Tyr | |
| | | 180 | | | | | 185 | | | | | 190 | | | | |
| GCG | GAG | CTG | GTG | TTG | GAG | CGC | GCC | CTG | GAC | CGA | GAA | CGG | GAG | CCT | AGT | 741 |
| Ala | Glu | Leu | Val | Leu | Glu | Arg | Ala | Leu | Asp | Arg | Glu | Arg | Glu | Pro | Ser | |
| | 195 | | | | | 200 | | | | | 205 | | | | | |
| CTC | CAG | TTA | GTG | CTG | ACG | GCG | TTG | GAC | GGA | GGG | ACC | CCA | GCT | CTC | TCC | 789 |
| Leu | Gln | Leu | Val | Leu | Thr | Ala | Leu | Asp | Gly | Gly | Thr | Pro | Ala | Leu | Ser | |
| 210 | | | | | 215 | | | | | 220 | | | | | 225 | |
| GCC | AGC | CTG | CCT | ATT | CAC | ATC | AAG | GTG | CTG | GAC | GCG | AAT | GAC | AAT | GCG | 837 |
| Ala | Ser | Leu | Pro | Ile | His | Ile | Lys | Val | Leu | Asp | Ala | Asn | Asp | Asn | Ala | |
| | | | 230 | | | | | | 235 | | | | | 240 | | |
| CCT | GTC | TTC | AAC | CAG | TCC | TTG | TAC | CGG | GCG | CGC | GTT | CCT | GGA | GGA | TGC | 885 |
| Pro | Val | Phe | Asn | Gln | Ser | Leu | Tyr | Arg | Ala | Arg | Val | Pro | Gly | Gly | Cys | |
| | | | 245 | | | | | 250 | | | | | 255 | | | |
| ACC | TCC | GGC | ACG | CGC | GTG | GTA | CAA | GTC | CTT | GCA | ACG | GAT | CTG | GAT | GAA | 933 |
| Thr | Ser | Gly | Thr | Arg | Val | Val | Gln | Val | Leu | Ala | Thr | Asp | Leu | Asp | Glu | |
| | | 260 | | | | | 265 | | | | | 270 | | | | |
| GGC | CCC | AAC | GGT | GAA | ATT | ATT | TAC | TCC | TTC | GGC | AGC | CAC | AAC | CGC | GCC | 981 |
| Gly | Pro | Asn | Gly | Glu | Ile | Ile | Tyr | Ser | Phe | Gly | Ser | His | Asn | Arg | Ala | |
| | 275 | | | | | 280 | | | | | 285 | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| GGC | GTG | CGG | CAA | CTA | TTC | GCC | TTA | GAC | CTT | GTA | ACC | GGG | ATG | CTG | ACA | 1029 |
| Gly | Val | Arg | Gln | Leu | Phe | Ala | Leu | Asp | Leu | Val | Thr | Gly | Met | Leu | Thr | |
| 290 | | | | | 295 | | | | | 300 | | | | | 305 | |
| ATC | AAG | GGT | CGG | CTG | GAC | TTC | GAG | GAC | ACC | AAA | CTC | CAT | GAG | ATT | TAC | 1077 |
| Ile | Lys | Gly | Arg | Leu | Asp | Phe | Glu | Asp | Thr | Lys | Leu | His | Glu | Ile | Tyr | |
| | | | | 310 | | | | | 315 | | | | | 320 | | |
| ATC | CAG | GCC | AAA | GAC | AAG | GGC | GCC | AAT | CCC | GAA | GGA | GCA | CAT | TGC | AAA | 1125 |
| Ile | Gln | Ala | Lys | Asp | Lys | Gly | Ala | Asn | Pro | Glu | Gly | Ala | His | Cys | Lys | |
| | | | 325 | | | | | 330 | | | | | 335 | | | |
| GTG | TTG | GTG | GAG | GTT | GTG | GAT | GTG | AAT | GAC | AAC | GCC | CCG | GAG | ATC | ACA | 1173 |
| Val | Leu | Val | Glu | Val | Val | Asp | Val | Asn | Asp | Asn | Ala | Pro | Glu | Ile | Thr | |
| | | 340 | | | | | 345 | | | | | 350 | | | | |
| GTC | ACC | TCC | GTG | TAC | AGC | CCA | GTA | CCC | GAG | GAT | GCC | TCT | GGG | ACT | GTC | 1221 |
| Val | Thr | Ser | Val | Tyr | Ser | Pro | Val | Pro | Glu | Asp | Ala | Ser | Gly | Thr | Val | |
| | 355 | | | | | 360 | | | | | 365 | | | | | |
| ATC | GCT | TTG | CTC | AGT | GTG | ACT | GAC | CTG | GAT | GCT | GGC | GAG | AAC | GGG | CTG | 1269 |
| Ile | Ala | Leu | Leu | Ser | Val | Thr | Asp | Leu | Asp | Ala | Gly | Glu | Asn | Gly | Leu | |
| 370 | | | | | 375 | | | | | 380 | | | | | 385 | |
| GTG | ACC | TGC | GAA | GTT | CCA | CCG | GGT | CTC | CCT | TTC | AGC | CTT | ACT | TCT | TCC | 1317 |
| Val | Thr | Cys | Glu | Val | Pro | Pro | Gly | Leu | Pro | Phe | Ser | Leu | Thr | Ser | Ser | |
| | | | | 390 | | | | | 395 | | | | | 400 | | |
| CTC | AAG | AAT | TAC | TTC | ACT | TTG | AAA | ACC | AGT | GCA | GAC | CTG | GAT | CGG | GAG | 1365 |
| Leu | Lys | Asn | Tyr | Phe | Thr | Leu | Lys | Thr | Ser | Ala | Asp | Leu | Asp | Arg | Glu | |
| | | | 405 | | | | | 410 | | | | | 415 | | | |
| ACT | GTG | CCA | GAA | TAC | AAC | CTC | AGC | ATC | ACC | GCC | CGA | GAC | GCC | GGA | ACC | 1413 |
| Thr | Val | Pro | Glu | Tyr | Asn | Leu | Ser | Ile | Thr | Ala | Arg | Asp | Ala | Gly | Thr | |
| | | 420 | | | | | 425 | | | | | 430 | | | | |
| CCT | TCC | CTC | TCA | GCC | CTT | ACA | ATA | GTG | CGT | GTT | CAA | GTG | TCC | GAC | ATC | 1461 |
| Pro | Ser | Leu | Ser | Ala | Leu | Thr | Ile | Val | Arg | Val | Gln | Val | Ser | Asp | Ile | |
| | 435 | | | | | 440 | | | | | 445 | | | | | |
| AAT | GAC | AAC | CCT | CCA | CAA | TCT | TCT | CAA | TCT | TCC | TAC | GAC | GTT | TAC | ATT | 1509 |
| Asn | Asp | Asn | Pro | Pro | Gln | Ser | Ser | Gln | Ser | Ser | Tyr | Asp | Val | Tyr | Ile | |
| 450 | | | | | 455 | | | | | 460 | | | | | 465 | |
| GAA | GAA | AAC | AAC | CTC | CCC | GGG | GCT | CCA | ATA | CTA | AAC | CTA | AGT | GTC | TGG | 1557 |
| Glu | Glu | Asn | Asn | Leu | Pro | Gly | Ala | Pro | Ile | Leu | Asn | Leu | Ser | Val | Trp | |
| | | | | 470 | | | | 475 | | | | | | 480 | | |
| GAC | CCC | GAC | GCC | CCG | CAG | AAT | GCT | CGG | CTT | TCT | TTC | TTT | CTC | TTG | GAG | 1605 |
| Asp | Pro | Asp | Ala | Pro | Gln | Asn | Ala | Arg | Leu | Ser | Phe | Phe | Leu | Leu | Glu | |
| | | | 485 | | | | | 490 | | | | | 495 | | | |
| CAA | GGA | GCT | GAA | ACC | GGG | CTA | GTG | GGT | CGC | TAT | TTC | ACA | ATA | AAT | CGT | 1653 |
| Gln | Gly | Ala | Glu | Thr | Gly | Leu | Val | Gly | Arg | Tyr | Phe | Thr | Ile | Asn | Arg | |
| | | 500 | | | | | 505 | | | | | 510 | | | | |
| GAC | AAT | GGC | ATA | GTG | TCA | TCC | TTA | GTG | CCC | CTA | GAC | TAT | GAG | GAT | CGG | 1701 |
| Asp | Asn | Gly | Ile | Val | Ser | Ser | Leu | Val | Pro | Leu | Asp | Tyr | Glu | Asp | Arg | |
| | 515 | | | | | 520 | | | | | 525 | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| CGG | GAA | TTT | GAA | TTA | ACA | GCT | CAT | ATC | AGC | GAT | GGG | GGC | ACC | CCG | GTC | 1749 |
| Arg | Glu | Phe | Glu | Leu | Thr | Ala | His | Ile | Ser | Asp | Gly | Gly | Thr | Pro | Val | |
| 530 | | | | | 535 | | | | | 540 | | | | | 545 | |
| CTA | GCC | ACC | AAC | ATC | AGC | GTG | AAC | ATA | TTT | GTC | ACT | GAT | CGC | AAT | GAC | 1797 |
| Leu | Ala | Thr | Asn | Ile | Ser | Val | Asn | Ile | Phe | Val | Thr | Asp | Arg | Asn | Asp | |
| | | | | 550 | | | | | 555 | | | | | 560 | | |
| AAT | GCC | CCC | CAG | GTC | CTA | TAT | CCT | CGG | CCA | GGT | GGG | AGC | TCG | GTG | GAG | 1845 |
| Asn | Ala | Pro | Gln | Val | Leu | Tyr | Pro | Arg | Pro | Gly | Gly | Ser | Ser | Val | Glu | |
| | | | 565 | | | | | 570 | | | | | 575 | | | |
| ATG | CTG | CCT | CGA | GGT | ACC | TCA | GCT | GGC | CAC | CTA | GTG | TCA | CGG | GTG | GTA | 1893 |
| Met | Leu | Pro | Arg | Gly | Thr | Ser | Ala | Gly | His | Leu | Val | Ser | Arg | Val | Val | |
| | | 580 | | | | | 585 | | | | | 590 | | | | |
| GGC | TGG | GAC | GCG | GAT | GCA | GGG | CAC | AAT | GCC | TGG | CTC | TCC | TAC | AGT | CTC | 1941 |
| Gly | Trp | Asp | Ala | Asp | Ala | Gly | His | Asn | Ala | Trp | Leu | Ser | Tyr | Ser | Leu | |
| | 595 | | | | | 600 | | | | | 605 | | | | | |
| TTT | GGA | TCC | CCT | AAC | CAG | AGC | CTT | TTT | GCC | ATA | GGG | CTG | CAC | ACT | GGT | 1989 |
| Phe | Gly | Ser | Pro | Asn | Gln | Ser | Leu | Phe | Ala | Ile | Gly | Leu | His | Thr | Gly | |
| 610 | | | | | 615 | | | | | 620 | | | | | 625 | |
| CAA | ATC | AGT | ACT | GCC | CGT | CCA | GTC | CAA | GAC | ACA | GAT | TCA | CCC | AGG | CAG | 2037 |
| Gln | Ile | Ser | Thr | Ala | Arg | Pro | Val | Gln | Asp | Thr | Asp | Ser | Pro | Arg | Gln | |
| | | | | 630 | | | | | 635 | | | | | 640 | | |
| ACT | CTC | ACT | GTC | TTG | ATC | AAA | GAC | AAT | GGG | GAG | CCT | TCG | CTC | TCC | ACC | 2085 |
| Thr | Leu | Thr | Val | Leu | Ile | Lys | Asp | Asn | Gly | Glu | Pro | Ser | Leu | Ser | Thr | |
| | | | 645 | | | | | 650 | | | | | 655 | | | |
| ACT | GCT | ACC | CTC | ACT | GTG | TCA | GTA | ACC | GAG | GAC | TCT | CCT | GAA | GCC | CGA | 2133 |
| Thr | Ala | Thr | Leu | Thr | Val | Ser | Val | Thr | Glu | Asp | Ser | Pro | Glu | Ala | Arg | |
| | | 660 | | | | | 665 | | | | | 670 | | | | |
| GCC | GAG | TTC | CCC | TCT | GGC | TCT | GCC | CCC | CGG | GAG | CAG | AAA | AAA | AAT | CTC | 2181 |
| Ala | Glu | Phe | Pro | Ser | Gly | Ser | Ala | Pro | Arg | Glu | Gln | Lys | Lys | Asn | Leu | |
| | 675 | | | | | 680 | | | | | 685 | | | | | |
| ACC | TTT | TAT | CTA | CTT | CTT | TCT | CTA | ATC | CTG | GTT | TCT | GTG | GGC | TTC | GTG | 2229 |
| Thr | Phe | Tyr | Leu | Leu | Ser | Leu | Ile | Leu | Val | Ser | Val | Gly | Phe | Val | | |
| 690 | | | | | 695 | | | | 700 | | | | | 705 | | |
| GTC | ACA | GTG | TTC | GGA | GTA | ATC | ATA | TTC | AAA | GTT | TAC | AAG | TGG | AAG | CAG | 2277 |
| Val | Thr | Val | Phe | Gly | Val | Ile | Ile | Phe | Lys | Val | Tyr | Lys | Trp | Lys | Gln | |
| | | | 710 | | | | | 715 | | | | | 720 | | | |
| TCT | AGA | GAC | CTA | TAC | CGA | GCC | CCG | GTG | AGC | TCA | CTG | TAC | CGA | ACA | CCA | 2325 |
| Ser | Arg | Asp | Leu | Tyr | Arg | Ala | Pro | Val | Ser | Ser | Leu | Tyr | Arg | Thr | Pro | |
| | | | 725 | | | | | 730 | | | | | 735 | | | |
| GGG | CCC | TCC | TTG | CAC | GCG | GAC | GCC | GTG | CGG | GGA | GGC | CTG | ATG | TCG | CCG | 2373 |
| Gly | Pro | Ser | Leu | His | Ala | Asp | Ala | Val | Arg | Gly | Gly | Leu | Met | Ser | Pro | |
| | | 740 | | | | | 745 | | | | | 750 | | | | |
| CAC | CTT | TAC | CAT | CAG | GTG | TAT | CTC | ACC | ACG | GAC | TCC | CGC | CGC | AGC | GAC | 2421 |
| His | Leu | Tyr | His | Gln | Val | Tyr | Leu | Thr | Thr | Asp | Ser | Arg | Arg | Ser | Asp | |
| | 755 | | | | | 760 | | | | | 765 | | | | | |

| | |
|--|------|
| CCG CTG CTG AAG AAA CCT GGT GCA GCC AGT CCA CTG GCC AGC CGC CAG | 2469 |
| Pro Leu Leu Lys Lys Pro Gly Ala Ala Ser Pro Leu Ala Ser Arg Gln | |
| 770 775 780 785 | |
| AAC ACG CTG CGG AGC TGT GAT CCG GTG TTC TAT AGG CAG GTG TTG GGT | 2517 |
| Asn Thr Leu Arg Ser Cys Asp Pro Val Phe Tyr Arg Gln Val Leu Gly | |
| 790 795 800 | |
| GCA GAG AGC GCC CCT CCC GGA CAG GTA AGG TTT AGC AAG TCA TGC TTG | 2565 |
| Ala Glu Ser Ala Pro Pro Gly Gln Val Arg Phe Ser Lys Ser Cys Leu | |
| 805 810 815 | |
| ACC CTG TTA GTG CCT TTT TAT TCC TAC ATC ATA TTG AGA AGG CTG GAG | 2613 |
| Thr Leu Leu Val Pro Phe Tyr Ser Tyr Ile Ile Leu Arg Arg Leu Glu | |
| 820 825 830 | |
| CTG TTT TTT TAGTGATGAA GATGTTTTCC TGGTGATGCA TTCACACTTT | 2662 |
| Leu Phe Phe | |
| 835 | |
| CAACTGGCTC TTCCTAGATC AAAGTTAGTG CCTTTGTGAG ATGGTGGCCT GCCAGAGTGT | 2722 |
| GGTTTGTGGT CCCATTTTCAG GGGGAAGATA CTTGACTCAT CTGTGGACCT AATTCACATC | 2782 |
| CTCAGCG | 2789 |

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 836 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

| | |
|---|--|
| Met Val Pro Glu Ala Trp Arg Ser Gly Leu Val Ser Thr Gly Arg Val | |
| 1 5 10 15 | |
| Val Gly Val Leu Leu Leu Gly Ala Leu Asn Lys Ala Ser Thr Val | |
| 20 25 30 | |
| Ile His Tyr Glu Ile Pro Glu Glu Arg Glu Lys Gly Phe Ala Val Gly | |
| 35 40 45 | |
| Asn Val Val Ala Asn Leu Gly Leu Asp Leu Gly Ser Leu Ser Ala Arg | |
| 50 55 60 | |
| Arg Phe Pro Val Val Ser Gly Ala Ser Arg Arg Phe Phe Glu Val Asn | |
| 65 70 75 80 | |
| Arg Glu Thr Gly Glu Met Phe Val Asn Asp Arg Leu Asp Arg Glu Glu | |
| 85 90 95 | |
| Leu Cys Gly Thr Leu Pro Ser Cys Thr Val Thr Leu Glu Leu Val Val | |
| 100 105 110 | |
| Glu Asn Pro Leu Glu Leu Phe Ser Val Glu Val Val Ile Gln Asp Ile | |
| 115 120 125 | |

| | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Asp | Asn | Asn | Pro | Ala | Phe | Pro | Thr | Gln | Glu | Met | Lys | Leu | Glu | Ile | 130 | 135 | 140 |
| Ser | Glu | Ala | Val | Ala | Pro | Gly | Thr | Arg | Phe | Pro | Leu | Glu | Ser | Ala | His | 145 | 150 | 155 |
| Asp | Pro | Asp | Leu | Gly | Ser | Asn | Ser | Leu | Gln | Thr | Tyr | Glu | Leu | Ser | Arg | 165 | 170 | 175 |
| Asn | Glu | Tyr | Phe | Ala | Leu | Arg | Val | Gln | Thr | Arg | Glu | Asp | Ser | Thr | Lys | 180 | 185 | 190 |
| Tyr | Ala | Glu | Leu | Val | Leu | Glu | Arg | Ala | Leu | Asp | Arg | Glu | Arg | Glu | Pro | 195 | 200 | 205 |
| Ser | Leu | Gln | Leu | Val | Leu | Thr | Ala | Leu | Asp | Gly | Gly | Thr | Pro | Ala | Leu | 210 | 215 | 220 |
| Ser | Ala | Ser | Leu | Pro | Ile | His | Ile | Lys | Val | Leu | Asp | Ala | Asn | Asp | Asn | 225 | 230 | 235 |
| Ala | Pro | Val | Phe | Asn | Gln | Ser | Leu | Tyr | Arg | Ala | Arg | Val | Pro | Gly | Gly | 245 | 250 | 255 |
| Cys | Thr | Ser | Gly | Thr | Arg | Val | Val | Gln | Val | Leu | Ala | Thr | Asp | Leu | Asp | 260 | 265 | 270 |
| Glu | Gly | Pro | Asn | Gly | Glu | Ile | Ile | Tyr | Ser | Phe | Gly | Ser | His | Asn | Arg | 275 | 280 | 285 |
| Ala | Gly | Val | Arg | Gln | Leu | Phe | Ala | Leu | Asp | Leu | Val | Thr | Gly | Met | Leu | 290 | 295 | 300 |
| Thr | Ile | Lys | Gly | Arg | Leu | Asp | Phe | Glu | Asp | Thr | Lys | Leu | His | Glu | Ile | 305 | 310 | 315 |
| Tyr | Ile | Gln | Ala | Lys | Asp | Lys | Gly | Ala | Asn | Pro | Glu | Gly | Ala | His | Cys | 325 | 330 | 335 |
| Lys | Val | Leu | Val | Glu | Val | Val | Asp | Val | Asn | Asp | Asn | Ala | Pro | Glu | Ile | 340 | 345 | 350 |
| Thr | Val | Thr | Ser | Val | Tyr | Ser | Pro | Val | Pro | Glu | Asp | Ala | Ser | Gly | Thr | 355 | 360 | 365 |
| Val | Ile | Ala | Leu | Leu | Ser | Val | Thr | Asp | Leu | Asp | Ala | Gly | Glu | Asn | Gly | 370 | 375 | 380 |
| Leu | Val | Thr | Cys | Glu | Val | Pro | Pro | Gly | Leu | Pro | Phe | Ser | Leu | Thr | Ser | 385 | 390 | 395 |
| Ser | Leu | Lys | Asn | Tyr | Phe | Thr | Leu | Lys | Thr | Ser | Ala | Asp | Leu | Asp | Arg | 405 | 410 | 415 |
| Glu | Thr | Val | Pro | Glu | Tyr | Asn | Leu | Ser | Ile | Thr | Ala | Arg | Asp | Ala | Gly | 420 | 425 | 430 |
| Thr | Pro | Ser | Leu | Ser | Ala | Leu | Thr | Ile | Val | Arg | Val | Gln | Val | Ser | Asp | 435 | 440 | 445 |
| Ile | Asn | Asp | Asn | Pro | Pro | Gln | Ser | Ser | Gln | Ser | Ser | Tyr | Asp | Val | Tyr | 450 | 455 | 460 |

Ile Glu Glu Asn Asn Leu Pro Gly Ala Pro Ile Leu Asn Leu Ser Val
465 470 475 480

Trp Asp Pro Asp Ala Pro Gln Asn Ala Arg Leu Ser Phe Phe Leu Leu
485 490 495

Glu Gln Gly Ala Glu Thr Gly Leu Val Gly Arg Tyr Phe Thr Ile Asn
500 505 510

Arg Asp Asn Gly Ile Val Ser Ser Leu Val Pro Leu Asp Tyr Glu Asp
515 520 525

Arg Arg Glu Phe Glu Leu Thr Ala His Ile Ser Asp Gly Gly Thr Pro
530 535 540

Val Leu Ala Thr Asn Ile Ser Val Asn Ile Phe Val Thr Asp Arg Asn
545 550 555 560

Asp Asn Ala Pro Gln Val Leu Tyr Pro Arg Pro Gly Gly Ser Ser Val
565 570 575

Glu Met Leu Pro Arg Gly Thr Ser Ala Gly His Leu Val Ser Arg Val
580 585 590

Val Gly Trp Asp Ala Asp Ala Gly His Asn Ala Trp Leu Ser Tyr Ser
595 600 605

Leu Phe Gly Ser Pro Asn Gln Ser Leu Phe Ala Ile Gly Leu His Thr
610 615 620

Gly Gln Ile Ser Thr Ala Arg Pro Val Gln Asp Thr Asp Ser Pro Arg
625 630 635 640

Gln Thr Leu Thr Val Leu Ile Lys Asp Asn Gly Glu Pro Ser Leu Ser
645 650 655

Thr Thr Ala Thr Leu Thr Val Ser Val Thr Glu Asp Ser Pro Glu Ala
660 665 670

Arg Ala Glu Phe Pro Ser Gly Ser Ala Pro Arg Glu Gln Lys Lys Asn
675 680 685

Leu Thr Phe Tyr Leu Leu Leu Ser Leu Ile Leu Val Ser Val Gly Phe
690 695 700

Val Val Thr Val Phe Gly Val Ile Ile Phe Lys Val Tyr Lys Trp Lys
705 710 715 720

Gln Ser Arg Asp Leu Tyr Arg Ala Pro Val Ser Ser Leu Tyr Arg Thr
725 730 735

Pro Gly Pro Ser Leu His Ala Asp Ala Val Arg Gly Gly Leu Met Ser
740 745 750

Pro His Leu Tyr His Gln Val Tyr Leu Thr Thr Asp Ser Arg Arg Ser
755 760 765

Asp Pro Leu Leu Lys Lys Pro Gly Ala Ala Ser Pro Leu Ala Ser Arg
770 775 780

Gln Asn Thr Leu Arg Ser Cys Asp Pro Val Phe Tyr Arg Gln Val Leu
785 790 795 800

Gly Ala Glu Ser Ala Pro Pro Gly Gln Val Arg Phe Ser Lys Ser Cys
805 810 815
Leu Thr Leu Leu Val Pro Phe Tyr Ser Tyr Ile Ile Leu Arg Arg Leu
820 825 830
Glu Leu Phe Phe
835

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2751 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 115..2160

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

| | |
|---|-----|
| CGAAAGCCAT GTCGGACTCG TCGCCAGCG CCAAGCGCT AACCCGCTGA AAGTTTCTCA | 60 |
| GCGAAATCTC AGGGACGATC TGGACCCGC TGAGAGGAAC TGCTTTTGAG TGAG ATG | 117 |
| Met | |
| 1 | |
| GTC CCA GAG GCC TGG AGG AGC GGA CTG GTA AGC ACC GGG AGG GTA GTG | 165 |
| Val Pro Glu Ala Trp Arg Ser Gly Leu Val Ser Thr Gly Arg Val Val | |
| 5 10 15 | |
| GGA GTT TTG CTT CTG CTT GGT GCC TTG AAC AAG GCT TCC ACG GTC ATT | 213 |
| Gly Val Leu Leu Leu Leu Gly Ala Leu Asn Lys Ala Ser Thr Val Ile | |
| 20 25 30 | |
| CAC TAT GAG ATC CCG GAG GAA AGA GAG AAG GGT TTC GCT GTG GGC AAC | 261 |
| His Tyr Glu Ile Pro Glu Glu Arg Glu Lys Gly Phe Ala Val Gly Asn | |
| 35 40 45 | |
| GTG GTC GCG AAC CTT GGT TTG GAT CTC GGT AGC CTC TCA GCC CGC AGG | 309 |
| Val Val Ala Asn Leu Gly Leu Asp Leu Gly Ser Leu Ser Ala Arg Arg | |
| 50 55 60 65 | |
| TTC CCG GTG GTG TCT GGA GCT AGC CGA AGA TTC TTT GAG GTG AAC CGG | 357 |
| Phe Pro Val Val Ser Gly Ala Ser Arg Arg Phe Phe Glu Val Asn Arg | |
| 70 75 80 | |
| GAG ACC GGA GAG ATG TTT GTG AAC GAC CGT CTG GAT CGA GAG GAG CTG | 405 |
| Glu Thr Gly Glu Met Phe Val Asn Asp Arg Leu Asp Arg Glu Glu Leu | |
| 85 90 95 | |
| TGT GGG ACA CTG CCC TCT TGC ACT GTA ACT CTG GAG TTG GTA GTG GAG | 453 |
| Cys Gly Thr Leu Pro Ser Cys Thr Val Thr Leu Glu Leu Val Val Glu | |
| 100 105 110 | |

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|-------------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------|
| AAC Asn 115 | CCG Pro | CTG Leu | GAG Glu | CTG Leu | TTC Phe | AGC Ser | GTG Val | GAA Glu | GTG Val | GTG Val | ATC Ile | CAG Gln | GAC Asp | ATC Ile | AAC Asn | 501 |
| GAC Asp 130 | AAC Asn | AAT Asn | CCT Pro | GCT Ala | TTC Phe | CCT Pro | ACC Thr | CAG Gln | GAA Glu | ATG Met | AAA Lys | TTG Leu | GAG Glu | ATT Ile | AGC Ser | 549 |
| GAG Glu | GCC Ala | GTG Val | GCT Ala | CCG Pro | GGG Gly | ACG Thr | CGC Arg | TTT Phe | CCG Pro | CTC Leu | GAG Glu | AGC Ser | GCG Ala | CAC His | GAT Asp | 597 |
| CCC Pro | GAT Asp | CTG Leu | GGA Gly | AGC Ser | AAC Asn | TCT Ser | TTA Leu | CAA Gln | ACC Thr | TAT Tyr | GAG Glu | CTG Leu | AGC Ser | CGA Arg | AAT Asn | 645 |
| GAA Glu | TAC Tyr | TTT Phe | GCG Ala | CTT Leu | CGC Arg | GTG Val | CAG Gln | ACG Thr | CGG Arg | GAG Glu | GAC Asp | AGC Ser | ACC Thr | AAG Lys | TAC Tyr | 693 |
| GCG Ala | GAG Glu | CTG Leu | GTG Val | TTG Leu | GAG Glu | CGC Arg | GCC Ala | CTG Leu | GAC Asp | CGA Arg | GAA Glu | CGG Arg | GAG Glu | CCT Pro | AGT Ser | 741 |
| CTC Leu | CAG Gln | TTA Leu | GTG Val | CTG Leu | ACG Thr | GCG Ala | TTG Leu | GAC Asp | GGA Gly | GGG Gly | ACC Thr | CCA Pro | GCT Ala | CTC Leu | TCC Ser | 789 |
| GCC Ala | AGC Ser | CTG Leu | CCT Pro | ATT Ile | CAC His | ATC Ile | AAG Lys | GTG Val | CTG Leu | GAC Asp | GCG Ala | AAT Asn | GAC Asp | AAT Asn | GCG Ala | 837 |
| CCT Pro | GTC Val | TTC Phe | AAC Asn | CAG Gln | TCC Ser | TTG Leu | TAC Tyr | CGG Arg | GCG Ala | CGC Arg | GTT Val | CCT Pro | GGA Gly | GGA Gly | TGC Cys | 885 |
| ACC Thr | TCC Ser | GGC Gly | ACG Thr | CGC Arg | GTG Val | GTA Val | CAA Gln | GTC Val | CTT Leu | GCA Ala | ACG Thr | GAT Asp | CTG Leu | GAT Asp | GAA Glu | 933 |
| GGC Gly | CCC Pro | AAC Asn | GGT Gly | GAA Glu | ATT Ile | ATT Ile | TAC Tyr | TCC Ser | TTC Phe | GGC Gly | AGC Ser | CAC His | AAC Asn | CGC Arg | GCC Ala | 981 |
| GGC Gly | GTG Val | CGG Arg | CAA Gln | CTA Leu | TTC Phe | GCC Ala | TTA Leu | GAC Asp | CTT Leu | GTA Val | ACC Thr | GGG Gly | ATG Met | CTG Leu | ACA Thr | 1029 |
| ATC Ile | AAG Lys | GGT Gly | CGG Arg | CTG Leu | GAC Asp | TTC Phe | GAG Glu | GAC Asp | ACC Thr | AAA Lys | CTC Leu | CAT His | GAG Glu | ATT Ile | TAC Tyr | 1077 |
| ATC Ile | CAG Gln | GCC Ala | AAA Lys | GAC Asp | AAG Lys | GGC Gly | GCC Ala | AAT Asn | CCC Pro | GAA Glu | GGA Gly | GCA Ala | CAT His | TGC Cys | AAA Lys | 1125 |
| GTG Val | TTG Leu | GTG Val | GAG Glu | GTT Val | GTG Val | GAT Asp | GTG Val | AAT Asn | GAC Asp | AAC Asn | GCC Ala | CCG Pro | GAG Glu | ATC Ile | ACA Thr | 1173 |

| | |
|---|------|
| GTC ACC TCC GTG TAC AGC CCA GTA CCC GAG GAT GCC TCT GGG ACT GTC | 1221 |
| Val Thr Ser Val Tyr Ser Pro Val Pro Glu Asp Ala Ser Gly Thr Val | |
| 355 360 365 | |
| ATC GCT TTG CTC AGT GTG ACT GAC CTG GAT GCT GGC GAG AAC GGG CTG | 1269 |
| Ile Ala Leu Leu Ser Val Thr Asp Leu Asp Ala Gly Glu Asn Gly Leu | |
| 370 375 380 385 | |
| GTG ACC TGC GAA GTT CCA CCG GGT CTC CCT TTC AGC CTT ACT TCT TCC | 1317 |
| Val Thr Cys Glu Val Pro Pro Gly Leu Pro Phe Ser Leu Thr Ser Ser | |
| 390 395 400 | |
| CTC AAG AAT TAC TTC ACT TTG AAA ACC AGT GCA GAC CTG GAT CGG GAG | 1365 |
| Leu Lys Asn Tyr Phe Thr Leu Lys Thr Ser Ala Asp Leu Asp Arg Glu | |
| 405 410 415 | |
| ACT GTG CCA GAA TAC AAC CTC AGC ATC ACC GCC CGA GAC GCC GGA ACC | 1413 |
| Thr Val Pro Glu Tyr Asn Leu Ser Ile Thr Ala Arg Asp Ala Gly Thr | |
| 420 425 430 | |
| CCT TCC CTC TCA GCC CTT ACA ATA GTG CGT GTT CAA GTG TCC GAC ATC | 1461 |
| Pro Ser Leu Ser Ala Leu Thr Ile Val Arg Val Gln Val Ser Asp Ile | |
| 435 440 445 | |
| AAT GAC AAC CCT CCA CAA TCT TCT CAA TCT TCC TAC GAC GTT TAC ATT | 1509 |
| Asn Asp Asn Pro Pro Gln Ser Ser Gln Ser Ser Tyr Asp Val Tyr Ile | |
| 450 455 460 465 | |
| GAA GAA AAC AAC CTC CCC GGG GCT CCA ATA CTA AAC CTA AGT GTC TGG | 1557 |
| Glu Glu Asn Asn Leu Pro Gly Ala Pro Ile Leu Asn Leu Ser Val Trp | |
| 470 475 480 | |
| GAC CCC GAC GCC CCG CAG AAT GCT CGG CTT TCT TTC TTT CTC TTG GAG | 1605 |
| Asp Pro Asp Ala Pro Gln Asn Ala Arg Leu Ser Phe Phe Leu Leu Glu | |
| 485 490 495 | |
| CAA GGA GCT GAA ACC GGG CTA GTG GGT CGC TAT TTC ACA ATA AAT CGT | 1653 |
| Gln Gly Ala Glu Thr Gly Leu Val Gly Arg Tyr Phe Thr Ile Asn Arg | |
| 500 505 510 | |
| GAC AAT GGC ATA GTG TCA TCC TTA GTG CCC CTA GAC TAT GAG GAT CGG | 1701 |
| Asp Asn Gly Ile Val Ser Ser Leu Val Pro Leu Asp Tyr Glu Asp Arg | |
| 515 520 525 | |
| CGG GAA TTT GAA TTA ACA GCT CAT ATC AGC GAT GGC GGC ACC CCG GTC | 1749 |
| Arg Glu Phe Glu Leu Thr Ala His Ile Ser Asp Gly Gly Thr Pro Val | |
| 530 535 540 545 | |
| CTA GCC ACC AAC ATC AGC GTG AAC ATA TTT GTC ACT GAT CGC AAT GAC | 1797 |
| Leu Ala Thr Asn Ile Ser Val Asn Ile Phe Val Thr Asp Arg Asn Asp | |
| 550 555 560 | |
| AAT GCC CCC CAG GTC CTA TAT CCT CGG CCA GGT GGG AGC TCG GTG GAG | 1845 |
| Asn Ala Pro Gln Val Leu Tyr Pro Arg Pro Gly Gly Ser Ser Val Glu | |
| 565 570 575 | |
| ATG CTG CCT CGA GGT ACC TCA GCT GGC CAC CTA GTG TCA CGG GTG GTA | 1893 |
| Met Leu Pro Arg Gly Thr Ser Ala Gly His Leu Val Ser Arg Val Val | |
| 580 585 590 | |

| | |
|---|------|
| GGC TGG GAC GCG GAT GCA GGG CAC AAT GCC TGG CTC TCC TAC AGT CTC | 1941 |
| Gly Trp Asp Ala Asp Ala Gly His Asn Ala Trp Leu Ser Tyr Ser Leu | |
| 595 600 605 | |
| TTT GGA TCC CCT AAC CAG AGC CTT TTT GCC ATA GGG CTG CAC ACT GGT | 1989 |
| Phe Gly Ser Pro Asn Gln Ser Leu Phe Ala Ile Gly Leu His Thr Gly | |
| 610 615 620 625 | |
| CAA ATC AGT ACT GCC CGT CCA GTC CAA GAC ACA GAT TCA CCC AGG CAG | 2037 |
| Gln Ile Ser Thr Ala Arg Pro Val Gln Asp Thr Asp Ser Pro Arg Gln | |
| 630 635 640 | |
| ACT CTC ACT GTC TTG ATC AAA GAC AAT GGG GAG CCT TCG CTC TCC ACC | 2085 |
| Thr Leu Thr Val Leu Ile Lys Asp Asn Gly Glu Pro Ser Leu Ser Thr | |
| 645 650 655 | |
| ACT GCT ACC CTC ACT GTG TCA GTA ACC GAG GAC TCT CCT GAA GCC CGA | 2133 |
| Thr Ala Thr Leu Thr Val Ser Val Thr Glu Asp Ser Pro Glu Ala Arg | |
| 660 665 670 | |
| GCC GAG TTC CCC TCT GGC TCT GCC AGT TAAACCTTCT TTAATTATGG | 2180 |
| Ala Glu Phe Pro Ser Gly Ser Ala Ser | |
| 675 680 | |
| ATTAGCCATT AACATTTTTTG AAACGTGGAC CATTTAACCT CGGCCTACCC CCTCCAAC TG | 2240 |
| TCCTGGTGAT GAGTTCATTA GCTAAGTTAA ATTAATTGAA CTTTGATCTA AACC AAAACA | 2300 |
| AATCAGGAAA ATAAAGCTGT AAAGGAACTT ATCAAGCATT CCAA AACCAA CTAGAAATTA | 2360 |
| CTTGAAGTTT CGAGTGAGCA TTGCCTGTGC CAGTATTCTT CATTATAGGA TTATAAACTC | 2420 |
| GTTTTTTTCC CAAAGCGCAT GTCTACGCCA GGCAGAGGAG TAATTATTCA GCCAATTTCA | 2480 |
| TGGATGTAAC GATGGATATA AATAATTGAT AGCACCTAGA GGCTTCCAGT TTGGGTGGAA | 2540 |
| GGCTAAAAGT AGAGGGGAAC TCACTCACTT GAGAAATGAT ATTTAAGTGA ATAAATAGTT | 2600 |
| CTCTTCTATG AAAC TATTAC TATTTAGTTC TCTGGAAAAC TTAAGTGTAT TAATGATTAG | 2660 |
| AACATCAAAT CCTAAGTAAA GAAATGACAT TTAAATATA AAAAGCCAAA CTTTAAATAA | 2720 |
| ATCATAGAGA CCTCAGACAT AATATAGGAA A | 2751 |

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 682 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

| | |
|---|--|
| Met Val Pro Glu Ala Trp Arg Ser Gly Leu Val Ser Thr Gly Arg Val | |
| 1 5 10 15 | |
| Val Gly Val Leu Leu Leu Gly Ala Leu Asn Lys Ala Ser Thr Val | |
| 20 25 30 | |

Ile His Tyr Glu Ile Pro Glu Glu Arg Glu Lys Gly Phe Ala Val Gly
35 40 45

Asn Val Val Ala Asn Leu Gly Leu Asp Leu Gly Ser Leu Ser Ala Arg
50 55 60

Arg Phe Pro Val Val Ser Gly Ala Ser Arg Arg Phe Phe Glu Val Asn
65 70 75 80

Arg Glu Thr Gly Glu Met Phe Val Asn Asp Arg Leu Asp Arg Glu Glu
85 90 95

Leu Cys Gly Thr Leu Pro Ser Cys Thr Val Thr Leu Glu Leu Val Val
100 105 110

Glu Asn Pro Leu Glu Leu Phe Ser Val Glu Val Val Ile Gln Asp Ile
115 120 125

Asn Asp Asn Asn Pro Ala Phe Pro Thr Gln Glu Met Lys Leu Glu Ile
130 135 140

Ser Glu Ala Val Ala Pro Gly Thr Arg Phe Pro Leu Glu Ser Ala His
145 150 155 160

Asp Pro Asp Leu Gly Ser Asn Ser Leu Gln Thr Tyr Glu Leu Ser Arg
165 170 175

Asn Glu Tyr Phe Ala Leu Arg Val Gln Thr Arg Glu Asp Ser Thr Lys
180 185 190

Tyr Ala Glu Leu Val Leu Glu Arg Ala Leu Asp Arg Glu Arg Glu Pro
195 200 205

Ser Leu Gln Leu Val Leu Thr Ala Leu Asp Gly Gly Thr Pro Ala Leu
210 215 220

Ser Ala Ser Leu Pro Ile His Ile Lys Val Leu Asp Ala Asn Asp Asn
225 230 235 240

Ala Pro Val Phe Asn Gln Ser Leu Tyr Arg Ala Arg Val Pro Gly Gly
245 250 255

Cys Thr Ser Gly Thr Arg Val Val Gln Val Leu Ala Thr Asp Leu Asp
260 265 270

Glu Gly Pro Asn Gly Glu Ile Ile Tyr Ser Phe Gly Ser His Asn Arg
275 280 285

Ala Gly Val Arg Gln Leu Phe Ala Leu Asp Leu Val Thr Gly Met Leu
290 295 300

Thr Ile Lys Gly Arg Leu Asp Phe Glu Asp Thr Lys Leu His Glu Ile
305 310 315 320

Tyr Ile Gln Ala Lys Asp Lys Gly Ala Asn Pro Glu Gly Ala His Cys
325 330 335

Lys Val Leu Val Glu Val Val Asp Val Asn Asp Asn Ala Pro Glu Ile
340 345 350

Thr Val Thr Ser Val Tyr Ser Pro Val Pro Glu Asp Ala Ser Gly Thr
355 360 365

Val Ile Ala Leu Leu Ser Val Thr Asp Leu Asp Ala Gly Glu Asn Gly
370 375 380

Leu Val Thr Cys Glu Val Pro Pro Gly Leu Pro Phe Ser Leu Thr Ser
385 390 395 400

Ser Leu Lys Asn Tyr Phe Thr Leu Lys Thr Ser Ala Asp Leu Asp Arg
405 410 415

Glu Thr Val Pro Glu Tyr Asn Leu Ser Ile Thr Ala Arg Asp Ala Gly
420 425 430

Thr Pro Ser Leu Ser Ala Leu Thr Ile Val Arg Val Gln Val Ser Asp
435 440 445

Ile Asn Asp Asn Pro Pro Gln Ser Ser Gln Ser Ser Tyr Asp Val Tyr
450 455 460

Ile Glu Glu Asn Asn Leu Pro Gly Ala Pro Ile Leu Asn Leu Ser Val
465 470 475 480

Trp Asp Pro Asp Ala Pro Gln Asn Ala Arg Leu Ser Phe Phe Leu Leu
485 490 495

Glu Gln Gly Ala Glu Thr Gly Leu Val Gly Arg Tyr Phe Thr Ile Asn
500 505 510

Arg Asp Asn Gly Ile Val Ser Ser Leu Val Pro Leu Asp Tyr Glu Asp
515 520 525

Arg Arg Glu Phe Glu Leu Thr Ala His Ile Ser Asp Gly Gly Thr Pro
530 535 540

Val Leu Ala Thr Asn Ile Ser Val Asn Ile Phe Val Thr Asp Arg Asn
545 550 555 560

Asp Asn Ala Pro Gln Val Leu Tyr Pro Arg Pro Gly Gly Ser Ser Val
565 570 575

Glu Met Leu Pro Arg Gly Thr Ser Ala Gly His Leu Val Ser Arg Val
580 585 590

Val Gly Trp Asp Ala Asp Ala Gly His Asn Ala Trp Leu Ser Tyr Ser
595 600 605

Leu Phe Gly Ser Pro Asn Gln Ser Leu Phe Ala Ile Gly Leu His Thr
610 615 620

Gly Gln Ile Ser Thr Ala Arg Pro Val Gln Asp Thr Asp Ser Pro Arg
625 630 635 640

Gln Thr Leu Thr Val Leu Ile Lys Asp Asn Gly Glu Pro Ser Leu Ser
645 650 655

Thr Thr Ala Thr Leu Thr Val Ser Val Thr Glu Asp Ser Pro Glu Ala
660 665 670

Arg Ala Glu Phe Pro Ser Gly Ser Ala Ser
675 680

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2831 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

| | |
|--|------|
| GAATTCGGCA CGAGGCTGAA CTGAGGGTGA CGGACATAAA CGACTATTCT CCAGTGTTCA | 60 |
| GTGAAAGAGA AATGATACTG AGGATACCAG AAAACAGTGC TCGGGGAAAT ACATTCCTTT | 120 |
| TAAACAATGC TCTGGACTCA GACGTAGATA TCAACAATAT CCAGACCTAT AGGCTCAGCT | 180 |
| CAAACCTCTCA TTTCCTGGTT GTAACCCGCA ACCGCAGTGA TGGCAGGAAG TACCCAGAGC | 240 |
| TGGTGCTGGA GAAAGAACTG GATCGAGAGG AGGAACCTGA GCTGAGGTTA ACGCTGACAG | 300 |
| CTTTGGATGG TGGCTCTCCT CCCCAGTCTG GGACGACACA GGTCCTCATT GAAGTAGTGG | 360 |
| ACACCAACGA TAATGCACCC GAGTTTCAGC AGCCAACATA CCAAGTGCAA ACTCCCGAGA | 420 |
| ACAGTCCCAC CGGCTCTCTG GTACTCACAG TCTCAGCCAA TGACTTAGAC AGTGGAGACT | 480 |
| ATGGGAAAGT CTTGTACGCA CTTTCGCAAC CCTCAGAAGA TATTAGCAAA ACATTCGAGG | 540 |
| TAAACCTGT AACCAGGGAA ATTTCGCTAC GAAAAGAGGT GAATTTTGAA ACTATTCCTT | 600 |
| CGTATGAAGT GGTTATCAAG GGGACGGACG GGGGAGGTCT CTCAGGAAAA TGCACTCTGT | 660 |
| TACTGCAGGT GGTGGACGTG AATGACAATG CCCAGAAGT GATGCTATCT GCGCTAACCA | 720 |
| ACCCAGTCCC AGAAAATTCC CCCGATGAGG TAGTGGCTGT TTTCAGTGTT AGAGATCCTG | 780 |
| ACTCTGGGAA CAACGGAAAA GTGATTGCAT CCATCGAGGA AGACCTGCCC TTTCTTCTAA | 840 |
| AATCTTCAGG AAAGAACTTT TACACTTTAG TAACCAAGGG AGCACTTGAC AGGGAAGAAA | 900 |
| GAGAGCAATT GAACATCACC ATCACAGTCA CTGACCTGGG CATACCCAGG CTCACCACCC | 960 |
| AACACACCAT AACAGTGCAG GTGGCAGACA TCAACGACAA TGCCCCCTCC TTCACCCAAA | 1020 |
| CCTCCTACAC CATGTTTGTC CGCGAGAACA ACAGCCCCGC CCTGCACATA GGCACCATCA | 1080 |
| GCGCCACAGA CTCAGACTCA GGATCCAATG CCCACATCAC CTACTCGCTG CTACCGCCCC | 1140 |
| AAGACCCACA GCTGGCCCTC GACTCGCTCA TCTCCATCAA TGTAGACAAC GGGCAGCTGT | 1200 |
| TCGCGCTCAG GCGCTAGAC TATGAGGCTC TGCAGGGCTT CGAGTTCCAT GTGGGCGCCA | 1260 |
| CAGACCAAGG CTCGCCCAGC CTCAGCAGCC AGGCTCTGGT GCACGTGGTG GTGTTGGACG | 1320 |
| ACAATGACAA TGCGCCCTTC GTGCTCTACC CGCTGCAAAA CGCCTCTGCA CCCTTCACTG | 1380 |
| AGCTGCTGCC CAGGGCGGCA GAGCCTGGAT ACCTGGTTAC CAAGGTGGTA GCTGTGGACC | 1440 |
| GCGACTCTGG CCAGAATGCC TGGCTGTCAT TCCAGCTGCT CAAGGCCACG GAGCCCGGGC | 1500 |

| | |
|--|------|
| TGTTCAACGT ATGGGCGCAC AATGGCGAGG TACGCACCTC CAGGCTGCTG AGCGAGCGCG | 1560 |
| ACGCACCCAA GCACAAGCTG CTGCTGTTGG TCAAGGACAA TGGAGATCCT CCACGCTCTG | 1620 |
| CCAGTGTAC TCTGCACGTG CTAGTGGTGG ATGCCCTTCTC TCAGCCCTAC CTGCCTCTGC | 1680 |
| CAGAGGTGGC GCACGACCCT GCACAAGAAG AAGATGCGCT AACACTCTAC CTGGTCATAG | 1740 |
| CTTTGGCATC TGTGTCTTCT CTCTTCCTCT TGTCTGTGCT GCTGTTTCGTG GGGGTGAGGC | 1800 |
| TCTGCAGGAG GGCCAGGGCA GCCTCTCTGA GTGCCATTTC TGTGCCTGAA GGCCACTTTC | 1860 |
| CTGGCCAGCT GGTGGATGTC AGAGGTATGG GGACCCTGTC CCAGAGCTAC CAGTATGATG | 1920 |
| TATGTCTGAT GGGGGATTCT TCTGGGACCA GCGAATTTAA CTTCTTAAAG CCAGTCTGTC | 1980 |
| CTAGCTCTCT GCACCAGTGC TCTGGGAAAG AAATAGAGGA AAATTCCACA CTCCAGAATA | 2040 |
| GTTTTGGGTT TCATCATTA TAGAAAACTA CTTTACAGAT ATTTAATTCC AAATATCATC | 2100 |
| TTGTTGATTA ACTAAAGTCT GTTCACATGT AGCTAGCTAG CAACGATTTT AATGTTCACT | 2160 |
| TTACCCATCT TTTTTCAGGG TCATGTCTAA AGCTACAAGT TTGNCTTTAC TTATACTTGT | 2220 |
| CGCACAGAAT NNNNNNNNNN TGGTGTATAA GTCACAGTCA TGGGATACTG GCACAAGATG | 2280 |
| GCAGCTTGAT TGCTCAGTTA TGGCTGCAAA GGGGNGCTTG AGTTTAGGGA ATGTGTTAGA | 2340 |
| GCTGGAATAA GTTTTCTGAG AAATGTGTAA GACAAATTTT TTTTGCACAT TCCCTGTGTT | 2400 |
| CCTGTACCCC TGTTTCCAGA ACTACGAAAT GTGTCATCAG AAGGCATGCT CACATTTTCC | 2460 |
| CCTTTGTTTG CGTGACCCGG GTGCCAGAAA TTAAATAAAA TTAGCATGGA GTTCAATGCA | 2520 |
| GCATTAAAAC AAAGTTACTT CTACAAACCT TTTATTCGAC GGTAAAAATT GTAACCTCCC | 2580 |
| CACCCATGAG GCTGGCTGTA AGAACCAGTA TGAATGGGTG TCTATCGCAA CCTTATTTTC | 2640 |
| AAAAATCAAA CAAAAGGAGA AATGAGAGAC CAAACAACAC GCTACAGGAA AGATTTTCATA | 2700 |
| AGGATGTATG TATGGACACA AAAACTGGGA TACAGACATT TTAAATCTGT TGGTACCACA | 2760 |
| TGGTGGCGCT GCAGGCTAAA GAAATGCAAG GGAAATTAAG AAGAGGCTGA GCTAGAAGTC | 2820 |
| AAAAAAAAA A | 2831 |

(2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3353 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS

(B) LOCATION: 763..3123

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

| | | | | | | |
|---|-------------|------------|------------|--------------------|------------|-----|
| GTATTTTTC | ACAGTTTAA | ATTTTCATA | AATCATAACT | CTCTGACTTT | ATGTAGAAAG | 60 |
| GATACCACAC | TGGAATTAAC | GTGTAGCTTT | TTCTTGATGT | AATCCAACCA | ATGGGAGCAC | 120 |
| AATTCTGGTA | CATAGGCTGT | CTAGAATTTG | AAAGAAATTA | AAGAATTCAT | TTTGTTTTGC | 180 |
| TGATAAATTT | TTAAGAAATC | ACGTGGCTTT | ATGTTATTAT | TATTACAAGA | TGACTGATCA | 240 |
| CTATTATGTC | TTCTTTTCACT | TCTCAATTTT | CCTCAGAACA | CTACACCCAG | ACTACAGGCT | 300 |
| CTGGAGGGTG | GGGACCATGT | CTGGGTTGTT | TACTGATGTA | TTTCATAATT | TGGCACATAG | 360 |
| AGACCAATAA | TACTCCTTTA | AATGAAGAAA | TTAATAATTA | CCATTGCGTG | ATATTGTGAT | 420 |
| TACATCATTT | CCTCCCAATT | TCCAAACTCC | TAATAGAATA | GAGAATAGAT | CAATTGTAGC | 480 |
| AATTCGTTTC | GAAGCAAAGA | CAACGCATGG | TGGCGCTGCA | GGCTAAGGCT | TCAAAAAGAG | 540 |
| GAAAAGGAAA | AAGCCCATGA | AATGCTACTA | GCTACTTCAG | ACCTCTTTCA | GCCTAAGAGG | 600 |
| AAAGCCTGTT | AGCAGAGCAC | GGACCAGTGT | CTCCGGAGAA | TGCTATTCTC | CTACATTTCC | 660 |
| GAACAGGTTA | TCAACGCACA | GATCGATCAC | TGCCTCTGTC | CCATCGCTCC | CTGAAGTAGC | 720 |
| TCTGACTCCG | GTTCTTGAA | AGGGGCGTGT | ACAGAAGTAA | AG ATG GAG CCT GCA | | 774 |
| | | | | Met Glu Pro Ala | | |
| | | | | 1 | | |
| GGG GAG CGC TTT CCC GAA CAA AGG CAA GTC CTG ATT CTC CTT CTT TTA | 822 | | | | | |
| Gly Glu Arg Phe Pro Glu Gln Arg Gln Val Leu Ile Leu Leu Leu Leu | | | | | | |
| 5 10 15 20 | | | | | | |
| CTG GAA GTG ACT CTG GCA GGC TGG GAA CCC CGT CGC TAT TCT GTG ATG | 870 | | | | | |
| Leu Glu Val Thr Leu Ala Gly Trp Glu Pro Arg Arg Tyr Ser Val Met | | | | | | |
| 25 30 35 | | | | | | |
| GAG GAA ACA GAG AGA GGT TCT TTT GTA GCC AAC CTG GCC AAT GAC CTA | 918 | | | | | |
| Glu Glu Thr Glu Arg Gly Ser Phe Val Ala Asn Leu Ala Asn Asp Leu | | | | | | |
| 40 45 50 | | | | | | |
| GGG CTG GGA GTG GGG GAG CTA GCC GAG CGG GGA GCC CGG GTA GTT TCT | 966 | | | | | |
| Gly Leu Gly Val Gly Glu Leu Ala Glu Arg Gly Ala Arg Val Val Ser | | | | | | |
| 55 60 65 | | | | | | |
| GAG GAT AAC GAA CAA GGC TTG CAG CTT GAT CTG CAG ACC GGG CAG TTG | 1014 | | | | | |
| Glu Asp Asn Glu Gln Gly Leu Gln Leu Asp Leu Gln Thr Gly Gln Leu | | | | | | |
| 70 75 80 | | | | | | |
| ATA TTA AAT GAG AAG CTG GAC CGG GAG AAG CTG TGT GGC CCT ACT GAG | 1062 | | | | | |
| Ile Leu Asn Glu Lys Leu Asp Arg Glu Lys Leu Cys Gly Pro Thr Glu | | | | | | |
| 85 90 95 100 | | | | | | |
| CCC TGT ATA ATG CAT TTC CAA GTG TTA CTG AAA AAA CCT TTG GAA GTA | 1110 | | | | | |
| Pro Cys Ile Met His Phe Gln Val Leu Leu Lys Lys Pro Leu Glu Val | | | | | | |
| 105 110 115 | | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| TTT | CGA | GCT | GAA | CTA | CTA | GTG | ACA | GAC | ATA | AAC | GAT | CAT | TCT | CCT | GAG | 1158 |
| Phe | Arg | Ala | Glu | Leu | Leu | Val | Thr | Asp | Ile | Asn | Asp | His | Ser | Pro | Glu | |
| | | | 120 | | | | | 125 | | | | | 130 | | | |
| TTT | CCT | GAA | AGA | GAA | ATG | ACC | CTG | AAA | ATC | CCA | GAA | ACT | AGC | TCC | CTT | 1206 |
| Phe | Pro | Glu | Arg | Glu | Met | Thr | Leu | Lys | Ile | Pro | Glu | Thr | Ser | Ser | Leu | |
| | | 135 | | | | | 140 | | | | | 145 | | | | |
| GGG | ACT | GTG | TTT | CCT | CTG | AAA | AAA | GCT | CGG | GAC | TTG | GAC | GTG | GGC | AGC | 1254 |
| Gly | Thr | Val | Phe | Pro | Leu | Lys | Lys | Ala | Arg | Asp | Leu | Asp | Val | Gly | Ser | |
| | 150 | | | | | 155 | | | | | 160 | | | | | |
| AAT | AAT | GTT | CAA | AAC | TAC | AAT | ATT | TCT | CCC | AAT | TCT | CAT | TTC | CAT | GTT | 1302 |
| Asn | Asn | Val | Gln | Asn | Tyr | Asn | Ile | Ser | Pro | Asn | Ser | His | Phe | His | Val | |
| 165 | | | | | 170 | | | | 175 | | | | | | 180 | |
| TCC | ACT | CGC | ACC | CGA | GGG | GAT | GGC | AGG | AAA | TAC | CCA | GAG | CTG | GTG | CTG | 1350 |
| Ser | Thr | Arg | Thr | Arg | Gly | Asp | Gly | Arg | Lys | Tyr | Pro | Glu | Leu | Val | Leu | |
| | | | | 185 | | | | | 190 | | | | | 195 | | |
| GAC | ACA | GAA | CTG | GAT | CGC | GAG | GAG | CAG | GCC | GAG | CTC | AGA | TTA | ACC | TTG | 1398 |
| Asp | Thr | Glu | Leu | Asp | Arg | Glu | Glu | Gln | Ala | Glu | Leu | Arg | Leu | Thr | Leu | |
| | | | 200 | | | | | 205 | | | | | 210 | | | |
| ACA | GCG | GTG | GAC | GGT | GGC | TCT | CCA | CCC | CGA | TCT | GGC | ACC | GTC | CAG | ATC | 1446 |
| Thr | Ala | Val | Asp | Gly | Gly | Ser | Pro | Pro | Arg | Ser | Gly | Thr | Val | Gln | Ile | |
| | | 215 | | | | | 220 | | | | | 225 | | | | |
| CTC | ATC | TTG | GTC | TTG | GAC | GCC | AAT | GAC | AAT | GCC | CCG | GAG | TTT | GTG | CAG | 1494 |
| Leu | Ile | Leu | Val | Leu | Asp | Ala | Asn | Asp | Asn | Ala | Pro | Glu | Phe | Val | Gln | |
| | 230 | | | | | 235 | | | | | 240 | | | | | |
| GCG | CTC | TAC | GAG | GTG | CAG | GTC | CCA | GAG | AAC | AGC | CCA | GTA | GGC | TCC | CTA | 1542 |
| Ala | Leu | Tyr | Glu | Val | Gln | Val | Pro | Glu | Asn | Ser | Pro | Val | Gly | Ser | Leu | |
| | 245 | | | | 250 | | | | | 255 | | | | | 260 | |
| GTT | GTC | AAG | GTC | TCT | GCT | AGG | GAT | TTA | GAC | ACT | GGG | ACA | AAT | GGA | GAG | 1590 |
| Val | Val | Lys | Val | Ser | Ala | Arg | Asp | Leu | Asp | Thr | Gly | Thr | Asn | Gly | Glu | |
| | | | | 265 | | | | | 270 | | | | | 275 | | |
| ATA | TCA | TAC | TCC | CTT | TAT | TAC | AGC | TCT | CAG | GAG | ATA | GAC | AAA | CCT | TTT | 1638 |
| Ile | Ser | Tyr | Ser | Leu | Tyr | Tyr | Ser | Ser | Gln | Glu | Ile | Asp | Lys | Pro | Phe | |
| | | | 280 | | | | | 285 | | | | | 290 | | | |
| GAG | CTA | AGC | AGC | CTT | TCA | GGA | GAA | ATT | CGA | CTA | ATT | AAA | AAA | CTA | GAT | 1686 |
| Glu | Leu | Ser | Ser | Leu | Ser | Gly | Glu | Ile | Arg | Leu | Ile | Lys | Lys | Leu | Asp | |
| | | 295 | | | | 300 | | | | | | 305 | | | | |
| TTT | GAG | ACA | ATG | TCT | TCA | TAT | GAT | CTA | GAT | ATA | GAG | GCA | TCT | GAT | GGC | 1734 |
| Phe | Glu | Thr | Met | Ser | Ser | Tyr | Asp | Leu | Asp | Ile | Glu | Ala | Ser | Asp | Gly | |
| | 310 | | | | | 315 | | | | | 320 | | | | | |
| GGG | GGA | CTT | TCT | GGA | AAA | TGC | TCT | GTC | TCT | GTT | AAG | GTG | CTG | GAT | GTT | 1782 |
| Gly | Gly | Leu | Ser | Gly | Lys | Cys | Ser | Val | Ser | Val | Lys | Val | Leu | Asp | Val | |
| | 325 | | | | 330 | | | | | 335 | | | | | 340 | |
| AAC | GAT | AAC | TTC | CCG | GAA | CTA | AGT | ATT | TCA | TCA | CTT | ACC | AGC | CCT | ATT | 1830 |
| Asn | Asp | Asn | Phe | Pro | Glu | Leu | Ser | Ile | Ser | Ser | Leu | Thr | Ser | Pro | Ile | |
| | | | | 345 | | | | | 350 | | | | | 355 | | |

| | | | | | | | | | | | | | | | | |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------|
| CCC Pro | GAG Glu | AAT Asn | TCT Ser | CCA Pro | GAG Glu | ACA Thr | GAA Glu | GTG Val | GCC Ala | CTG Leu | TTT Phe | AGG Arg | ATT Ile | AGA Arg | GAC Asp | 1878 |
| | | 360 | | | | | | 365 | | | | | 370 | | | |
| CGA Arg | GAC Asp | TCT Ser | GGA Gly | GAA Glu | AAT Asn | GGA Gly | AAA Lys | ATG Met | ATT Ile | TGC Cys | TCA Ser | ATT Ile | CAG Gln | GAT Asp | GAT Asp | 1926 |
| | | 375 | | | | | 380 | | | | | 385 | | | | |
| GTT Val | CCT Pro | TTT Phe | AAG Lys | CTA Leu | AAA Lys | CCT Pro | TCT Ser | GTT Val | GAG Glu | AAT Asn | TTC Phe | TAC Tyr | AGG Arg | CTG Leu | GTA Val | 1974 |
| | 390 | | | | | 395 | | | | | 400 | | | | | |
| ACA Thr | GAA Glu | GGG Gly | GCG Ala | CTG Leu | GAC Asp | AGA Arg | GAG Glu | ACC Thr | AGA Arg | GCC Ala | GAG Glu | TAC Tyr | AAC Asn | ATC Ile | ACC Thr | 2022 |
| | 405 | | | | 410 | | | | | 415 | | | | | 420 | |
| ATC Ile | ACC Thr | ATC Ile | ACA Thr | GAC Asp | TTG Leu | GGG Gly | ACT Thr | CCA Pro | AGG Arg | CTG Leu | AAA Lys | ACC Thr | GAG Glu | CAG Gln | AGC Ser | 2070 |
| | | | | 425 | | | | | 430 | | | | | 435 | | |
| ATA Ile | ACC Thr | GTG Val | CTG Leu | GTG Val | TCG Ser | GAC Asp | GTC Val | AAT Asn | GAC Asp | AAC Asn | GCC Ala | CCC Pro | GCC Ala | TTC Phe | ACC Thr | 2118 |
| | | | 440 | | | | | 445 | | | | | 450 | | | |
| CAA Gln | ACC Thr | TCC Ser | TAC Tyr | ACC Thr | CTG Leu | TTC Phe | GTC Val | CGC Arg | GAG Glu | AAC Asn | AAC Asn | AGC Ser | CCC Pro | GCC Ala | CTG Leu | 2166 |
| | | 455 | | | | | 460 | | | | | 465 | | | | |
| CAC His | ATC Ile | GGC Gly | AGT Ser | GTC Val | AGC Ser | GCC Ala | ACA Thr | GAC Asp | AGA Arg | GAC Asp | TCG Ser | GGC Gly | ACC Thr | AAC Asn | GCC Ala | 2214 |
| | 470 | | | | | 475 | | | | | 480 | | | | | |
| CAG Gln | GTC Val | ACC Thr | TAC Tyr | TCG Ser | CTG Leu | CTG Leu | CCG Pro | CCC Pro | CAG Gln | GAC Asp | CCG Pro | CAC His | CTG Leu | CCC Pro | CTA Leu | 2262 |
| | 485 | | | | 490 | | | | | 495 | | | | | 500 | |
| ACC Thr | TCC Ser | CTG Leu | GTC Val | TCC Ser | ATT Ile | AAC Asn | ACG Thr | GAC Asp | AAC Asn | GGC Gly | CAC His | CTG Leu | TTC Phe | GCT Ala | CTC Leu | 2310 |
| | | | | 505 | | | | | 510 | | | | | 515 | | |
| CAG Gln | TCG Ser | CTG Leu | GAC Asp | TAC Tyr | GAG Glu | GCC Ala | CTG Leu | CAG Gln | GCT Ala | TTC Phe | GAG Glu | TTC Phe | CGC Arg | GTG Val | GGC Gly | 2358 |
| | | | 520 | | | | | 525 | | | | | 530 | | | |
| GCC Ala | ACA Thr | GAC Asp | CGC Arg | GGC Gly | TTC Phe | CCG Pro | GCG Ala | CTG Leu | AGC Ser | AGC Ser | GAG Glu | GCG Ala | CTG Leu | GTG Val | CGA Arg | 2406 |
| | | 535 | | | | | 540 | | | | | 545 | | | | |
| GTG Val | CTG Leu | GTG Val | CTG Leu | GAC Asp | GCC Ala | AAC Asn | GAC Asp | AAC Asn | TCG Ser | CCC Pro | TTC Phe | GTG Val | CTG Leu | TAC Tyr | CCG Pro | 2454 |
| | | 550 | | | | 555 | | | | | 560 | | | | | |
| CTG Leu | CAG Gln | AAC Asn | GGC Gly | TCC Ser | GCG Ala | CCC Pro | TGC Cys | ACC Thr | GAG Glu | CTG Leu | GTG Val | CCC Pro | CGG Arg | GCG Ala | GCC Ala | 2502 |
| | 565 | | | | 570 | | | | | 575 | | | | | 580 | |
| GAG Glu | CCG Pro | GGC Gly | TAC Tyr | CTG Leu | GTG Val | ACC Thr | AAG Lys | GTG Val | GTG Val | GCG Ala | GTG Val | GAC Asp | GGC Gly | GAC Asp | TCG Ser | 2550 |
| | | | | 585 | | | | | 590 | | | | | 595 | | |

| | |
|---|------|
| GGC CAG AAC GCC TGG CTG TCG TAC CAG CTG CTC AAG GCC ACG GAG CCC | 2598 |
| Gly Gln Asn Ala Trp Leu Ser Tyr Gln Leu Leu Lys Ala Thr Glu Pro | |
| 600 605 610 | |
| GGG CTG TTC GGC GTG TGG GCG CAC AAT GGC GAG GTG CGC ACC GCC AGG | 2646 |
| Gly Leu Phe Gly Val Trp Ala His Asn Gly Glu Val Arg Thr Ala Arg | |
| 615 620 625 | |
| CTG CTG AGC GAG CGC GAC GTG GCC AAG CAC AGG CTA GTG GTG CTG GTC | 2694 |
| Leu Leu Ser Glu Arg Asp Val Ala Lys His Arg Leu Val Val Leu Val | |
| 630 635 640 | |
| AAG GAC AAT GGC GAG CCT CCG CGC TCG GCC ACA GCC ACG CTG CAA GTG | 2742 |
| Lys Asp Asn Gly Glu Pro Pro Arg Ser Ala Thr Ala Thr Leu Gln Val | |
| 645 650 655 660 | |
| CTC CTG GTG GAC GGC TTC TCT CAG CCC TAC CTG CCG CTC CCA GAG GCG | 2790 |
| Leu Leu Val Asp Gly Phe Ser Gln Pro Tyr Leu Pro Leu Pro Glu Ala | |
| 665 670 675 | |
| GCC CCG GCC CAA GCC CAG GCC GAC TCG CTT ACC GTC TAC CTG GTG GTG | 2838 |
| Ala Pro Ala Gln Ala Gln Ala Asp Ser Leu Thr Val Tyr Leu Val Val | |
| 680 685 690 | |
| GCA TTG GCC TCG GTG TCT TCG CTC TTC CTC TTC TCG GTG TTC CTG TTC | 2886 |
| Ala Leu Ala Ser Val Ser Ser Leu Phe Leu Phe Ser Val Phe Leu Phe | |
| 695 700 705 | |
| GTG GCA GTG CGG CTG TGC AGG AGG AGC AGG GCG GCC TCA GTG GGT CGC | 2934 |
| Val Ala Val Arg Leu Cys Arg Arg Ser Arg Ala Ala Ser Val Gly Arg | |
| 710 715 720 | |
| TGC TCG GTG CCC GAG GGC CCC TTT CCA GGG CAT CTG GTG GAC GTG AGC | 2982 |
| Cys Ser Val Pro Glu Gly Pro Phe Pro Gly His Leu Val Asp Val Ser | |
| 725 730 735 740 | |
| GGC ACC GGG ACC CTT TCC CAG AGC TAC CAG TAC GAG GTG TGT CTG ACG | 3030 |
| Gly Thr Gly Thr Leu Ser Gln Ser Tyr Gln Tyr Glu Val Cys Leu Thr | |
| 745 750 755 | |
| GGA GGC TCT GAA AGT AAT GAT TTC AAG TTC TTG AAG CCT ATA TTC CCA | 3078 |
| Gly Gly Ser Glu Ser Asn Asp Phe Lys Phe Leu Lys Pro Ile Phe Pro | |
| 760 765 770 | |
| AAT ATT GTA AGC CAG GAC TCT AGG AGG AAA TCA GAA TTT CTA GAA | 3123 |
| Asn Ile Val Ser Gln Asp Ser Arg Arg Lys Ser Glu Phe Leu Glu | |
| 775 780 785 | |
| TAATGTAGGT ATCTGTAGCT TTCCGACCGT CTGTTAATTT TGTCTTCCTC ACTTTTCACC | 3183 |
| TTAGTTTTTT TTAACCCTTT AGTAATCTTG AATTCTACTT TTTTTTAAAT TTCTACTGTT | 3243 |
| GTCTTTAGTA ATGTTACTCA TTTCTTTTGT CTGATTGTGA GTTTTCAAAT TATTGTATTA | 3303 |
| TTATAAATAT TTTATATCAG GAAAGTTCAT ATTTCTGAAT AAATTAATAG | 3353 |

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 787 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Glu | Pro | Ala | Gly | Glu | Arg | Phe | Pro | Glu | Gln | Arg | Gln | Val | Leu | Ile | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| Leu | Leu | Leu | Leu | Leu | Glu | Val | Thr | Leu | Ala | Gly | Trp | Glu | Pro | Arg | Arg | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| Tyr | Ser | Val | Met | Glu | Glu | Thr | Glu | Arg | Gly | Ser | Phe | Val | Ala | Asn | Leu | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |
| Ala | Asn | Asp | Leu | Gly | Leu | Gly | Val | Gly | Glu | Leu | Ala | Glu | Arg | Gly | Ala | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| Arg | Val | Val | Ser | Glu | Asp | Asn | Glu | Gln | Gly | Leu | Gln | Leu | Asp | Leu | Gln | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | |
| Thr | Gly | Gln | Leu | Ile | Leu | Asn | Glu | Lys | Leu | Asp | Arg | Glu | Lys | Leu | Cys | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| Gly | Pro | Thr | Glu | Pro | Cys | Ile | Met | His | Phe | Gln | Val | Leu | Leu | Lys | Lys | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| Pro | Leu | Glu | Val | Phe | Arg | Ala | Glu | Leu | Leu | Val | Thr | Asp | Ile | Asn | Asp | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| His | Ser | Pro | Glu | Phe | Pro | Glu | Arg | Glu | Met | Thr | Leu | Lys | Ile | Pro | Glu | |
| | | 130 | | | | 135 | | | | | 140 | | | | | |
| Thr | Ser | Ser | Leu | Gly | Thr | Val | Phe | Pro | Leu | Lys | Lys | Ala | Arg | Asp | Leu | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| Asp | Val | Gly | Ser | Asn | Asn | Val | Gln | Asn | Tyr | Asn | Ile | Ser | Pro | Asn | Ser | |
| | | | | 165 | | | | | 170 | | | | | 175 | | |
| His | Phe | His | Val | Ser | Thr | Arg | Thr | Arg | Gly | Asp | Gly | Arg | Lys | Tyr | Pro | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| Glu | Leu | Val | Leu | Asp | Thr | Glu | Leu | Asp | Arg | Glu | Glu | Gln | Ala | Glu | Leu | |
| | | 195 | | | | | 200 | | | | | 205 | | | | |
| Arg | Leu | Thr | Leu | Thr | Ala | Val | Asp | Gly | Gly | Ser | Pro | Pro | Arg | Ser | Gly | |
| | 210 | | | | | 215 | | | | | 220 | | | | | |
| Thr | Val | Gln | Ile | Leu | Ile | Leu | Val | Leu | Asp | Ala | Asn | Asp | Asn | Ala | Pro | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | |
| Glu | Phe | Val | Gln | Ala | Leu | Tyr | Glu | Val | Gln | Val | Pro | Glu | Asn | Ser | Pro | |
| | | | | 245 | | | | | 250 | | | | 255 | | | |
| Val | Gly | Ser | Leu | Val | Val | Lys | Val | Ser | Ala | Arg | Asp | Leu | Asp | Thr | Gly | |
| | | | 260 | | | | | 265 | | | | | 270 | | | |
| Thr | Asn | Gly | Glu | Ile | Ser | Tyr | Ser | Leu | Tyr | Tyr | Ser | Ser | Gln | Glu | Ile | |
| | | 275 | | | | | 280 | | | | | 285 | | | | |

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Lys | Pro | Phe | Glu | Leu | Ser | Ser | Leu | Ser | Gly | Glu | Ile | Arg | Leu | Ile | 290 | 295 | 300 | |
| Lys | Lys | Leu | Asp | Phe | Glu | Thr | Met | Ser | Ser | Tyr | Asp | Leu | Asp | Ile | Glu | 305 | 310 | 315 | 320 |
| Ala | Ser | Asp | Gly | Gly | Gly | Leu | Ser | Gly | Lys | Cys | Ser | Val | Ser | Val | Lys | 325 | 330 | 335 | |
| Val | Leu | Asp | Val | Asn | Asp | Asn | Phe | Pro | Glu | Leu | Ser | Ile | Ser | Ser | Leu | 340 | 345 | 350 | |
| Thr | Ser | Pro | Ile | Pro | Glu | Asn | Ser | Pro | Glu | Thr | Glu | Val | Ala | Leu | Phe | 355 | 360 | 365 | |
| Arg | Ile | Arg | Asp | Arg | Asp | Ser | Gly | Glu | Asn | Gly | Lys | Met | Ile | Cys | Ser | 370 | 375 | 380 | |
| Ile | Gln | Asp | Asp | Val | Pro | Phe | Lys | Leu | Lys | Pro | Ser | Val | Glu | Asn | Phe | 385 | 390 | 395 | 400 |
| Tyr | Arg | Leu | Val | Thr | Glu | Gly | Ala | Leu | Asp | Arg | Glu | Thr | Arg | Ala | Glu | 405 | 410 | 415 | |
| Tyr | Asn | Ile | Thr | Ile | Thr | Ile | Thr | Asp | Leu | Gly | Thr | Pro | Arg | Leu | Lys | 420 | 425 | 430 | |
| Thr | Glu | Gln | Ser | Ile | Thr | Val | Leu | Val | Ser | Asp | Val | Asn | Asp | Asn | Ala | 435 | 440 | 445 | |
| Pro | Ala | Phe | Thr | Gln | Thr | Ser | Tyr | Thr | Leu | Phe | Val | Arg | Glu | Asn | Asn | 450 | 455 | 460 | |
| Ser | Pro | Ala | Leu | His | Ile | Gly | Ser | Val | Ser | Ala | Thr | Asp | Arg | Asp | Ser | 465 | 470 | 475 | 480 |
| Gly | Thr | Asn | Ala | Gln | Val | Thr | Tyr | Ser | Leu | Leu | Pro | Pro | Gln | Asp | Pro | 485 | 490 | 495 | |
| His | Leu | Pro | Leu | Thr | Ser | Leu | Val | Ser | Ile | Asn | Thr | Asp | Asn | Gly | His | 500 | 505 | 510 | |
| Leu | Phe | Ala | Leu | Gln | Ser | Leu | Asp | Tyr | Glu | Ala | Leu | Gln | Ala | Phe | Glu | 515 | 520 | 525 | |
| Phe | Arg | Val | Gly | Ala | Thr | Asp | Arg | Gly | Phe | Pro | Ala | Leu | Ser | Ser | Glu | 530 | 535 | 540 | |
| Ala | Leu | Val | Arg | Val | Leu | Val | Leu | Asp | Ala | Asn | Asp | Asn | Ser | Pro | Phe | 545 | 550 | 555 | 560 |
| Val | Leu | Tyr | Pro | Leu | Gln | Asn | Gly | Ser | Ala | Pro | Cys | Thr | Glu | Leu | Val | 565 | 570 | 575 | |
| Pro | Arg | Ala | Ala | Glu | Pro | Gly | Tyr | Leu | Val | Thr | Lys | Val | Val | Ala | Val | 580 | 585 | 590 | |
| Asp | Gly | Asp | Ser | Gly | Gln | Asn | Ala | Trp | Leu | Ser | Tyr | Gln | Leu | Leu | Lys | 595 | 600 | 605 | |

Ala Thr Glu Pro Gly Leu Phe Gly Val Trp Ala His Asn Gly Glu Val
610 615 620

Arg Thr Ala Arg Leu Leu Ser Glu Arg Asp Val Ala Lys His Arg Leu
625 630 635 640

Val Val Leu Val Lys Asp Asn Gly Glu Pro Pro Arg Ser Ala Thr Ala
645 650 655

Thr Leu Gln Val Leu Leu Val Asp Gly Phe Ser Gln Pro Tyr Leu Pro
660 665 670

Leu Pro Glu Ala Ala Pro Ala Gln Ala Gln Ala Asp Ser Leu Thr Val
675 680 685

Tyr Leu Val Val Ala Leu Ala Ser Val Ser Ser Leu Phe Leu Phe Ser
690 695 700

Val Phe Leu Phe Val Ala Val Arg Leu Cys Arg Arg Ser Arg Ala Ala
705 710 715 720

Ser Val Gly Arg Cys Ser Val Pro Glu Gly Pro Phe Pro Gly His Leu
725 730 735

Val Asp Val Ser Gly Thr Gly Thr Leu Ser Gln Ser Tyr Gln Tyr Glu
740 745 750

Val Cys Leu Thr Gly Gly Ser Glu Ser Asn Asp Phe Lys Phe Leu Lys
755 760 765

Pro Ile Phe Pro Asn Ile Val Ser Gln Asp Ser Arg Arg Lys Ser Glu
770 775 780

Phe Leu Glu
785

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3033 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 138..2528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

| | |
|---|-----|
| GTGATTGGAC GTGTTTTTGT GACTATTTGG GAAGAAGACA CCTTCCTAAT CAGATTTACT | 60 |
| CCAATATCTT CCCGGACCCT CATGAGTGGA TTGCAATTGA CTTGAAGAAG CAGCACCTC | 120 |
| AGGACTGAAT CTGAACA ATG GAG ACA GCA CTA GCA AAA ATA CCA CAG CAA | 170 |
| Met Glu Thr Ala Leu Ala Lys Ile Pro Gln Gln | |
| 1 5 10 | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AGG | CAA | GTC | TTT | TTT | CTT | ACT | ATA | TTG | TCG | TTA | TTG | TGG | AAG | TCT | AGC | 218 |
| Arg | Gln | Val | Phe | Phe | Leu | Thr | Ile | Leu | Ser | Leu | Leu | Trp | Lys | Ser | Ser | |
| | | | 15 | | | | | 20 | | | | | 25 | | | |
| TCT | GAG | GCC | ATT | AGA | TAT | TCC | ATG | CCA | GAA | GAA | ACA | GAG | AGT | GGC | TAT | 266 |
| Ser | Glu | Ala | Ile | Arg | Tyr | Ser | Met | Pro | Glu | Glu | Thr | Glu | Ser | Gly | Tyr | |
| | | 30 | | | | | 35 | | | | | 40 | | | | |
| ATG | GTG | GCT | AAC | CTG | GCG | AAA | GAT | CTG | GGG | ATC | AGG | GTT | GGA | GAA | CTG | 314 |
| Met | Val | Ala | Asn | Leu | Ala | Lys | Asp | Leu | Gly | Ile | Arg | Val | Gly | Glu | Leu | |
| | 45 | | | | | 50 | | | | | 55 | | | | | |
| TCC | TCT | AGA | GGA | GCT | CAA | ATC | CAT | TAC | AAA | GGA | AAC | AAA | GAA | CTT | TTG | 362 |
| Ser | Ser | Arg | Gly | Ala | Gln | Ile | His | Tyr | Lys | Gly | Asn | Lys | Glu | Leu | Leu | |
| | 60 | | | | 65 | | | | | 70 | | | | | 75 | |
| CAG | CTG | GAT | GCA | GAG | ACT | GGG | AAT | TTG | TTC | TTA | AAG | GAA | AAA | CTA | GAC | 410 |
| Gln | Leu | Asp | Ala | Glu | Thr | Gly | Asn | Leu | Phe | Leu | Lys | Glu | Lys | Leu | Asp | |
| | | | | 80 | | | | | 85 | | | | | 90 | | |
| AGA | GAA | CTG | CTG | TGT | GGA | GAG | ACA | GAA | CCC | TGT | GTG | CTG | AAC | TTC | CAG | 458 |
| Arg | Glu | Leu | Leu | Cys | Gly | Glu | Thr | Glu | Pro | Cys | Val | Leu | Asn | Phe | Gln | |
| | | | 95 | | | | | 100 | | | | | 105 | | | |
| ATC | ATA | CTG | GAA | AAC | CCT | ATG | CAG | TTC | TTC | CAA | ACT | GAA | CTG | CAG | CTC | 506 |
| Ile | Ile | Leu | Glu | Asn | Pro | Met | Gln | Phe | Phe | Gln | Thr | Glu | Leu | Gln | Leu | |
| | | 110 | | | | | 115 | | | | | 120 | | | | |
| ACA | GAT | ATA | AAC | GAC | CAT | TCT | CCA | GAG | TTC | CCC | AAC | AAG | AAA | ATG | CTT | 554 |
| Thr | Asp | Ile | Asn | Asp | His | Ser | Pro | Glu | Phe | Pro | Asn | Lys | Lys | Met | Leu | |
| | 125 | | | | | 130 | | | | | 135 | | | | | |
| CTA | ACA | ATT | CCT | GAG | AGT | GCC | CAT | CCA | GGG | ACT | GTG | TTT | CCT | CTG | AAG | 602 |
| Leu | Thr | Ile | Pro | Glu | Ser | Ala | His | Pro | Gly | Thr | Val | Phe | Pro | Leu | Lys | |
| | 140 | | | | | 145 | | | | 150 | | | | | 155 | |
| GCA | GCT | CGG | GAC | TCT | GAC | ATA | GGG | AGC | AAC | GCT | GTT | CAG | AAC | TAC | ACA | 650 |
| Ala | Ala | Arg | Asp | Ser | Asp | Ile | Gly | Ser | Asn | Ala | Val | Gln | Asn | Tyr | Thr | |
| | | | | 160 | | | | | 165 | | | | | 170 | | |
| GTC | AAT | CCC | AAC | CTC | CAT | TTC | CAC | GTC | GTT | ACT | CAC | AGT | CGC | ACA | GAT | 698 |
| Val | Asn | Pro | Asn | Leu | His | Phe | His | Val | Val | Thr | His | Ser | Arg | Thr | Asp | |
| | | | 175 | | | | | 180 | | | | | 185 | | | |
| GGC | AGG | AAA | TAC | CCA | GAG | CTG | GTG | CTG | GAC | AGA | GCC | CTG | GAT | AGG | GAG | 746 |
| Gly | Arg | Lys | Tyr | Pro | Glu | Leu | Val | Leu | Asp | Arg | Ala | Leu | Asp | Arg | Glu | |
| | | 190 | | | | | 195 | | | | | 200 | | | | |
| GAG | CAG | CCT | GAG | CTC | ACT | TTA | ATC | CTC | ACT | GCT | CTG | GAT | GGT | GGA | GCT | 794 |
| Glu | Gln | Pro | Glu | Leu | Thr | Leu | Ile | Leu | Thr | Ala | Leu | Asp | Gly | Gly | Ala | |
| | | 205 | | | | 210 | | | | | 215 | | | | | |
| CCT | TCC | AGG | TCA | GGA | ACC | ACC | ACA | GTT | CAC | ATA | GAA | GTT | GTG | GAC | ATC | 842 |
| Pro | Ser | Arg | Ser | Gly | Thr | Thr | Thr | Val | His | Ile | Glu | Val | Val | Asp | Ile | |
| | | | | | 225 | | | | | 230 | | | | | 235 | |
| AAT | GAT | AAC | TCC | CCC | CAG | TTT | GTA | CAG | TCA | CTC | TAT | AAG | GTG | CAA | GTT | 890 |
| Asn | Asp | Asn | Ser | Pro | Gln | Phe | Val | Gln | Ser | Leu | Tyr | Lys | Val | Gln | Val | |
| | | | | 240 | | | | | 245 | | | | | 250 | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| CCT | GAG | AAT | AAT | CCC | CTC | AAT | GCC | TTT | GTT | GTC | ACG | GTC | TCT | GCC | ACG | 938 |
| Pro | Glu | Asn | Asn | Pro | Leu | Asn | Ala | Phe | Val | Val | Thr | Val | Ser | Ala | Thr | |
| | | 255 | | | | | | 260 | | | | | 265 | | | |
| GAT | TTA | GAT | GCT | GGG | GTA | TAT | GGC | AAT | GTG | ACC | TAT | TCT | CTG | TTT | CAA | 986 |
| Asp | Leu | Asp | Ala | Gly | Val | Tyr | Gly | Asn | Val | Thr | Tyr | Ser | Leu | Phe | Gln | |
| | | 270 | | | | | 275 | | | | | 280 | | | | |
| GGG | TAT | GGG | GTA | TTT | CAA | CCA | TTT | GTA | ATA | GAC | GAA | ATC | ACT | GGA | GAA | 1034 |
| Gly | Tyr | Gly | Val | Phe | Gln | Pro | Phe | Val | Ile | Asp | Glu | Ile | Thr | Gly | Glu | |
| | 285 | | | | | 290 | | | | | 295 | | | | | |
| ATC | CAT | CTG | AGC | AAA | GAG | CTG | GAT | TTT | GAG | GAA | ATT | AGC | AAT | CAT | AAC | 1082 |
| Ile | His | Leu | Ser | Lys | Glu | Leu | Asp | Phe | Glu | Glu | Ile | Ser | Asn | His | Asn | |
| 300 | | | | | 305 | | | | | 310 | | | | | 315 | |
| ATA | GAA | ATC | GCA | GCC | ACA | GAT | GGA | GGA | GGC | CTT | TCA | GGA | AAA | TGC | ACT | 1130 |
| Ile | Glu | Ile | Ala | Ala | Thr | Asp | Gly | Gly | Gly | Leu | Ser | Gly | Lys | Cys | Thr | |
| | | | | 320 | | | | | 325 | | | | | 330 | | |
| GTG | GCT | GTA | CAG | GTG | TTG | GAT | GTG | AAT | GAC | AAC | GCC | CCA | GAG | TTG | ACA | 1178 |
| Val | Ala | Val | Gln | Val | Leu | Asp | Val | Asn | Asp | Asn | Ala | Pro | Glu | Leu | Thr | |
| | | | 335 | | | | | 340 | | | | | 345 | | | |
| ATT | AGG | AAG | CTC | ACA | GTC | CTG | GTC | CCA | GAA | AAT | TCC | GCA | GAG | ACT | GTA | 1226 |
| Ile | Arg | Lys | Leu | Thr | Val | Leu | Val | Pro | Glu | Asn | Ser | Ala | Glu | Thr | Val | |
| | | 350 | | | | | 355 | | | | | 360 | | | | |
| GTT | GCT | GTT | TTT | AGT | GTT | TCT | GAT | TCT | GAT | TCG | GGG | GAC | AAT | GGA | AGG | 1274 |
| Val | Ala | Val | Phe | Ser | Val | Ser | Asp | Ser | Asp | Ser | Gly | Asp | Asn | Gly | Arg | |
| | 365 | | | | | 370 | | | | | 375 | | | | | |
| ATG | GTG | TGT | TCT | ATT | CCG | AAC | AAT | ATC | CCA | TTT | CTC | CTG | AAA | CCC | ACA | 1322 |
| Met | Val | Cys | Ser | Ile | Pro | Asn | Asn | Ile | Pro | Phe | Leu | Leu | Lys | Pro | Thr | |
| 380 | | | | | 385 | | | | | 390 | | | | | 395 | |
| TTT | GAG | AAT | TAT | TAC | ACG | TTA | GTG | ACT | GAG | GGG | CCA | CTT | GAT | AGA | GAG | 1370 |
| Phe | Glu | Asn | Tyr | Tyr | Thr | Leu | Val | Thr | Glu | Gly | Pro | Leu | Asp | Arg | Glu | |
| | | | 400 | | | | | | 405 | | | | | 410 | | |
| AAC | AGA | GCT | GAG | TAC | AAC | ATC | ACC | ATC | ACG | GTC | TCA | GAT | CTG | GGC | ACA | 1418 |
| Asn | Arg | Ala | Glu | Tyr | Asn | Ile | Thr | Ile | Thr | Val | Ser | Asp | Leu | Gly | Thr | |
| | | | 415 | | | | | 420 | | | | | 425 | | | |
| CCC | AGG | CTC | ACA | ACC | CAG | CAC | ACC | ATA | ACA | GTG | CAA | GTG | TCC | GAC | ATC | 1466 |
| Pro | Arg | Leu | Thr | Thr | Gln | His | Thr | Ile | Thr | Val | Gln | Val | Ser | Asp | Ile | |
| | | 430 | | | | | 435 | | | | | 440 | | | | |
| AAC | GAC | AAC | GCC | CCT | GCC | TTC | ACC | CAA | ACC | TCC | TAC | ACC | ATG | TTT | GTC | 1514 |
| Asn | Asp | Asn | Ala | Pro | Ala | Phe | Thr | Gln | Thr | Ser | Tyr | Thr | Met | Phe | Val | |
| | 445 | | | | | 450 | | | | | 455 | | | | | |
| CAC | GAG | AAC | AAC | AGC | CCC | GCC | CTG | CAC | ATA | GGC | ACC | ATC | AGT | GCC | ACA | 1562 |
| His | Glu | Asn | Asn | Ser | Pro | Ala | Leu | His | Ile | Gly | Thr | Ile | Ser | Ala | Thr | |
| 460 | | | | | 465 | | | | | 470 | | | | | 475 | |
| GAC | TCA | GAC | TCA | GGC | TCC | AAT | GCC | CAC | ATC | ACC | TAC | TCG | CTG | CTG | CCG | 1610 |
| Asp | Ser | Asp | Ser | Gly | Ser | Asn | Ala | His | Ile | Thr | Tyr | Ser | Leu | Leu | Pro | |
| | | | | 480 | | | | | 485 | | | | | | 490 | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| CCT | GAT | GAC | CCG | CAG | CTG | GCC | CTC | GAC | TCA | CTC | ATC | TCC | ATC | AAT | GTT | 1658 |
| Pro | Asp | Asp | Pro | Gln | Leu | Ala | Leu | Asp | Ser | Leu | Ile | Ser | Ile | Asn | Val | |
| | | | 495 | | | | | 500 | | | | | 505 | | | |
| GAC | AAT | GGG | CAG | CTG | TTC | GCG | CTC | AGA | GCT | CTA | GAC | TAT | GAG | GCA | CTG | 1706 |
| Asp | Asn | Gly | Gln | Leu | Phe | Ala | Leu | Arg | Ala | Leu | Asp | Tyr | Glu | Ala | Leu | |
| | | 510 | | | | | 515 | | | | | 520 | | | | |
| CAG | TCC | TTC | GAG | TTC | TAC | GTG | GGC | GCT | ACA | GAT | GGA | GGC | TCA | CCC | GCG | 1754 |
| Gln | Ser | Phe | Glu | Phe | Tyr | Val | Gly | Ala | Thr | Asp | Gly | Gly | Ser | Pro | Ala | |
| | 525 | | | | | 530 | | | | | 535 | | | | | |
| CTC | AGC | AGC | CAG | ACT | CTG | GTG | CGG | ATG | GTG | GTG | CTG | GAT | GAC | AAT | GAC | 1802 |
| Leu | Ser | Ser | Gln | Thr | Leu | Val | Arg | Met | Val | Val | Leu | Asp | Asp | Asn | Asp | |
| 540 | | | | | 545 | | | | | 550 | | | | | 555 | |
| AAT | GCC | CCC | TTC | GTG | CTC | TAC | CCA | CTG | CAG | AAT | GCC | TCA | GCA | CCC | TGT | 1850 |
| Asn | Ala | Pro | Phe | Val | Leu | Tyr | Pro | Leu | Gln | Asn | Ala | Ser | Ala | Pro | Cys | |
| | | | | 560 | | | | | 565 | | | | | 570 | | |
| ACT | GAG | CTA | CTG | CCT | AGG | GCA | GCA | GAG | CCC | GGC | TAC | CTG | ATC | ACC | AAA | 1898 |
| Thr | Glu | Leu | Leu | Pro | Arg | Ala | Ala | Glu | Pro | Gly | Tyr | Leu | Ile | Thr | Lys | |
| | | | 575 | | | | | 580 | | | | | 585 | | | |
| GTG | GTG | GCT | GTG | GAT | CGC | GAC | TCT | GGA | CAG | AAT | GCT | TGG | CTG | TCG | TTC | 1946 |
| Val | Val | Ala | Val | Asp | Arg | Asp | Ser | Gly | Gln | Asn | Ala | Trp | Leu | Ser | Phe | |
| | | 590 | | | | | 595 | | | | | 600 | | | | |
| CAG | CTA | CTT | AAA | GCT | ACA | GAG | CCA | GGG | CTG | TTC | AGT | GTA | TGG | GCA | CAC | 1994 |
| Gln | Leu | Leu | Lys | Ala | Thr | Glu | Pro | Gly | Leu | Phe | Ser | Val | Trp | Ala | His | |
| | 605 | | | | | 610 | | | | | 615 | | | | | |
| AAT | GGT | GAA | GTG | CGC | ACC | ACT | AGG | CTG | CTG | AGT | GAG | CGA | GAT | GCT | CAG | 2042 |
| Asn | Gly | Glu | Val | Arg | Thr | Thr | Arg | Leu | Leu | Ser | Glu | Arg | Asp | Ala | Gln | |
| 620 | | | | | 625 | | | | | 630 | | | | | 635 | |
| AAG | CAC | AAG | CTA | CTG | CTG | CTG | GTC | AAG | GAC | AAT | GGC | GAT | CCT | CTG | CGC | 2090 |
| Lys | His | Lys | Leu | Leu | Leu | Leu | Val | Lys | Asp | Asn | Gly | Asp | Pro | Leu | Arg | |
| | | | | 640 | | | | | 645 | | | | | 650 | | |
| TCT | GCC | AAT | GTC | ACT | CTT | CAC | GTG | CTA | GTG | GTG | GAT | GGC | TTC | TCG | CAG | 2138 |
| Ser | Ala | Asn | Val | Thr | Leu | His | Val | Leu | Val | Val | Asp | Gly | Phe | Ser | Gln | |
| | | | 655 | | | | | 660 | | | | | 665 | | | |
| CCT | TAC | CTA | CCA | TTG | GCT | GAG | GTG | GCA | CAG | GAT | TCC | ATG | CAA | GAT | AAT | 2186 |
| Pro | Tyr | Leu | Pro | Leu | Ala | Glu | Val | Ala | Gln | Asp | Ser | Met | Gln | Asp | Asn | |
| | | 670 | | | | | 675 | | | | | 680 | | | | |
| TAC | GAC | GTT | CTC | ACA | CTG | TAC | CTA | GTC | ATT | GCC | TTG | GCA | TCT | GTA | TCT | 2234 |
| Tyr | Asp | Val | Leu | Thr | Leu | Tyr | Leu | Val | Ile | Ala | Leu | Ala | Ser | Val | Ser | |
| | 685 | | | | | 690 | | | | | 695 | | | | | |
| TCT | CTC | TTC | CTC | TTG | TCT | GTA | GTG | CTG | TTT | GTG | GGG | GTG | AGG | CTG | TGC | 2282 |
| Ser | Leu | Phe | Leu | Leu | Ser | Val | Val | Leu | Phe | Val | Gly | Val | Arg | Leu | Cys | |
| 700 | | | | | 705 | | | | | 710 | | | | | 715 | |
| AGG | AGG | GCC | AGG | GAG | GCC | TCC | TTG | GGT | GAC | TAC | TCT | GTG | CCT | GAG | GGA | 2330 |
| Arg | Arg | Ala | Arg | Glu | Ala | Ser | Leu | Gly | Asp | Tyr | Ser | Val | Pro | Glu | Gly | |
| | | | | 720 | | | | | 725 | | | | | 730 | | |
| CAC | TTT | CCT | AGC | CAC | TTG | GTG | GAT | GTC | AGC | GGT | GCC | GGG | ACC | CTG | TCC | 2378 |

| | | | | | | | | | | | | | | | | | |
|------------|-------------|------------|-------------|------------|------------|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|------|
| His | Phe | Pro | Ser | His | Leu | Val | Asp | Val | Ser | Gly | Ala | Gly | Thr | Leu | Ser | | |
| | | | 735 | | | | | 740 | | | | | 745 | | | | |
| CAG | AGT | TAT | CAA | TAT | GAG | GTG | TGT | CTT | AAT | GGA | GGT | ACT | AGA | ACA | AAT | | 2426 |
| Gln | Ser | Tyr | Gln | Tyr | Glu | Val | Cys | Leu | Asn | Gly | Gly | Thr | Arg | Thr | Asn | | |
| | | 750 | | | | | 755 | | | | | 760 | | | | | |
| GAG | TTT | AAC | TTT | CTT | AAA | CCA | TTG | TTT | CCT | ATC | CTT | CCG | ACC | CAG | GCT | | 2474 |
| Glu | Phe | Asn | Phe | Leu | Lys | Pro | Leu | Phe | Pro | Ile | Leu | Pro | Thr | Gln | Ala | | |
| | 765 | | | | | 770 | | | | | 775 | | | | | | |
| GCT | GCT | GCT | GAA | GAA | AGA | GAA | AAC | GCT | GTT | GTG | CAC | AAT | AGC | GTT | GGA | | 2522 |
| Ala | Ala | Ala | Glu | Glu | Arg | Glu | Asn | Ala | Val | Val | His | Asn | Ser | Val | Gly | | |
| 780 | | | | | 785 | | | | 790 | | | | | 795 | | | |
| TTC | TAT | TAGAGCACTG | ATTTTGAAGT | GGTGGTTACC | TCATTTTTC | TTAACTATCC | | | | | | | | | | | 2578 |
| Phe | Tyr | | | | | | | | | | | | | | | | |
| CTGATGTAGA | ATGGTGTAGT | GCCGTGAATC | AACTCCTGAG | ATATATGTTT | ATTTTATCCT | | | | | | | | | | | | 2638 |
| TTGTTTTGAA | TCAAACCTATT | CAGATGTGAT | CCTACTCTAG | AGAATTTGGT | TCTACTCCAT | | | | | | | | | | | | 2698 |
| TGTGTTTGTT | TAGATTTCTA | CGCCATACCA | GTGCATGCTG | GGTGTGTTTT | TTTTTTACAA | | | | | | | | | | | | 2758 |
| TTATTATAAC | TTTGCTTTGG | AGGGGAACTC | ATATTCGCTG | TAACGAATTG | GAACCACTTT | | | | | | | | | | | | 2818 |
| CATTGTTAGA | GATGCCTTGC | TTTGTTGTGT | TATTTTCAGAC | AGGGTCTTAA | ATTGTAGCCC | | | | | | | | | | | | 2878 |
| TGGGTGACCT | GAAATGACTA | TGTACAGACT | GACTTTGAAT | TTGTGGCAGT | CCATCTGCCT | | | | | | | | | | | | 2938 |
| CTGTTGTCCT | ATGTTGGGAT | TGTGAGCATG | CATGAGTAGG | CTCAGCTGTG | GTGAGCGACC | | | | | | | | | | | | 2998 |
| TTAATAAAAA | TCAAATACTA | AAAAAAAAAA | AAAAA | | | | | | | | | | | | | | 3033 |

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 797 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Met | Glu | Thr | Ala | Leu | Ala | Lys | Ile | Pro | Gln | Gln | Arg | Gln | Val | Phe | Phe | | |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | | | |
| Leu | Thr | Ile | Leu | Ser | Leu | Leu | Trp | Lys | Ser | Ser | Ser | Glu | Ala | Ile | Arg | | |
| | | | 20 | | | | | 25 | | | | | 30 | | | | |
| Tyr | Ser | Met | Pro | Glu | Glu | Thr | Glu | Ser | Gly | Tyr | Met | Val | Ala | Asn | Leu | | |
| | | 35 | | | | | 40 | | | | | 45 | | | | | |
| Ala | Lys | Asp | Leu | Gly | Ile | Arg | Val | Gly | Glu | Leu | Ser | Ser | Arg | Gly | Ala | | |
| | 50 | | | | | 55 | | | | | 60 | | | | | | |
| Gln | Ile | His | Tyr | Lys | Gly | Asn | Lys | Glu | Leu | Leu | Gln | Leu | Asp | Ala | Glu | | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Gly | Asn | Leu | Phe | Leu | Lys | Glu | Lys | Leu | Asp | Arg | Glu | Leu | Leu | Cys |
| | | | 85 | | | | | | 90 | | | | | 95 | |
| Gly | Glu | Thr | Glu | Pro | Cys | Val | Leu | Asn | Phe | Gln | Ile | Ile | Leu | Glu | Asn |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Pro | Met | Gln | Phe | Phe | Gln | Thr | Glu | Leu | Gln | Leu | Thr | Asp | Ile | Asn | Asp |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| His | Ser | Pro | Glu | Phe | Pro | Asn | Lys | Lys | Met | Leu | Leu | Thr | Ile | Pro | Glu |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Ser | Ala | His | Pro | Gly | Thr | Val | Phe | Pro | Leu | Lys | Ala | Ala | Arg | Asp | Ser |
| 145 | | | | | 150 | | | | | 155 | | | | 160 | |
| Asp | Ile | Gly | Ser | Asn | Ala | Val | Gln | Asn | Tyr | Thr | Val | Asn | Pro | Asn | Leu |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| His | Phe | His | Val | Val | Thr | His | Ser | Arg | Thr | Asp | Gly | Arg | Lys | Tyr | Pro |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Glu | Leu | Val | Leu | Asp | Arg | Ala | Leu | Asp | Arg | Glu | Glu | Gln | Pro | Glu | Leu |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Thr | Leu | Ile | Leu | Thr | Ala | Leu | Asp | Gly | Gly | Ala | Pro | Ser | Arg | Ser | Gly |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Thr | Thr | Thr | Val | His | Ile | Glu | Val | Val | Asp | Ile | Asn | Asp | Asn | Ser | Pro |
| 225 | | | | 230 | | | | | | 235 | | | | 240 | |
| Gln | Phe | Val | Gln | Ser | Leu | Tyr | Lys | Val | Gln | Val | Pro | Glu | Asn | Asn | Pro |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Leu | Asn | Ala | Phe | Val | Val | Thr | Val | Ser | Ala | Thr | Asp | Leu | Asp | Ala | Gly |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Val | Tyr | Gly | Asn | Val | Thr | Tyr | Ser | Leu | Phe | Gln | Gly | Tyr | Gly | Val | Phe |
| | | 275 | | | | | 280 | | | | | 285 | | | |
| Gln | Pro | Phe | Val | Ile | Asp | Glu | Ile | Thr | Gly | Glu | Ile | His | Leu | Ser | Lys |
| | 290 | | | | | 295 | | | | | 300 | | | | |
| Glu | Leu | Asp | Phe | Glu | Glu | Ile | Ser | Asn | His | Asn | Ile | Glu | Ile | Ala | Ala |
| 305 | | | | | 310 | | | | | 315 | | | | 320 | |
| Thr | Asp | Gly | Gly | Gly | Leu | Ser | Gly | Lys | Cys | Thr | Val | Ala | Val | Gln | Val |
| | | | | 325 | | | | | 330 | | | | | 335 | |
| Leu | Asp | Val | Asn | Asp | Asn | Ala | Pro | Glu | Leu | Thr | Ile | Arg | Lys | Leu | Thr |
| | | | 340 | | | | | 345 | | | | | 350 | | |
| Val | Leu | Val | Pro | Glu | Asn | Ser | Ala | Glu | Thr | Val | Val | Ala | Val | Phe | Ser |
| | | 355 | | | | | 360 | | | | | 365 | | | |
| Val | Ser | Asp | Ser | Asp | Ser | Gly | Asp | Asn | Gly | Arg | Met | Val | Cys | Ser | Ile |
| | 370 | | | | | 375 | | | | 380 | | | | | |
| Pro | Asn | Asn | Ile | Pro | Phe | Leu | Leu | Lys | Pro | Thr | Phe | Glu | Asn | Tyr | Tyr |
| 385 | | | | | 390 | | | | | 395 | | | | 400 | |

Thr Leu Val Thr Glu Gly Pro Leu Asp Arg Glu Asn Arg Ala Glu Tyr
405 410 415

Asn Ile Thr Ile Thr Val Ser Asp Leu Gly Thr Pro Arg Leu Thr Thr
420 425 430

Gln His Thr Ile Thr Val Gln Val Ser Asp Ile Asn Asp Asn Ala Pro
435 440 445

Ala Phe Thr Gln Thr Ser Tyr Thr Met Phe Val His Glu Asn Asn Ser
450 455 460

Pro Ala Leu His Ile Gly Thr Ile Ser Ala Thr Asp Ser Asp Ser Gly
465 470 475 480

Ser Asn Ala His Ile Thr Tyr Ser Leu Leu Pro Pro Asp Asp Pro Gln
485 490 495

Leu Ala Leu Asp Ser Leu Ile Ser Ile Asn Val Asp Asn Gly Gln Leu
500 505 510

Phe Ala Leu Arg Ala Leu Asp Tyr Glu Ala Leu Gln Ser Phe Glu Phe
515 520 525

Tyr Val Gly Ala Thr Asp Gly Gly Ser Pro Ala Leu Ser Ser Gln Thr
530 535 540

Leu Val Arg Met Val Val Leu Asp Asp Asn Asp Asn Ala Pro Phe Val
545 550 555 560

Leu Tyr Pro Leu Gln Asn Ala Ser Ala Pro Cys Thr Glu Leu Leu Pro
565 570 575

Arg Ala Ala Glu Pro Gly Tyr Leu Ile Thr Lys Val Val Ala Val Asp
580 585 590

Arg Asp Ser Gly Gln Asn Ala Trp Leu Ser Phe Gln Leu Leu Lys Ala
595 600 605

Thr Glu Pro Gly Leu Phe Ser Val Trp Ala His Asn Gly Glu Val Arg
610 615 620

Thr Thr Arg Leu Leu Ser Glu Arg Asp Ala Gln Lys His Lys Leu Leu
625 630 635 640

Leu Leu Val Lys Asp Asn Gly Asp Pro Leu Arg Ser Ala Asn Val Thr
645 650 655

Leu His Val Leu Val Val Asp Gly Phe Ser Gln Pro Tyr Leu Pro Leu
660 665 670

Ala Glu Val Ala Gln Asp Ser Met Gln Asp Asn Tyr Asp Val Leu Thr
675 680 685

Leu Tyr Leu Val Ile Ala Leu Ala Ser Val Ser Ser Leu Phe Leu Leu
690 695 700

Ser Val Val Leu Phe Val Gly Val Arg Leu Cys Arg Arg Ala Arg Glu
705 710 715 720

Ala Ser Leu Gly Asp Tyr Ser Val Pro Glu Gly His Phe Pro Ser His
725 730 735

Leu Val Asp Val Ser Gly Ala Gly Thr Leu Ser Gln Ser Tyr Gln Tyr
740 745 750

Glu Val Cys Leu Asn Gly Gly Thr Arg Thr Asn Glu Phe Asn Phe Leu
755 760 765

Lys Pro Leu Phe Pro Ile Leu Pro Thr Gln Ala Ala Ala Ala Glu Glu
770 775 780

Arg Glu Asn Ala Val Val His Asn Ser Val Gly Phe Tyr
785 790 795

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2347 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

| | |
|---|------|
| AAAACACGGG GGAAATGACA GTAGCAAAGA ATCTGGACTA TGAAGAATGC TCATTGTATG | 60 |
| AAATGGAAAT ACAGGCTGAA GATGTGGGGG CGCTTCTGGG GAGGAGCAAA GTGGTAATTA | 120 |
| TGGTAGAAGA TGTAATGAC AATCGGCCAG AAGTGACCAT TACATCCTTG TTTAACCCGG | 180 |
| TATTGGAAAA TTCTCTTCCC GGGACAGTAA TTGCCTTCTT GAATGTGCAT GACCGAGACT | 240 |
| CTGGAAAGAA CGGCCAAGTT GTCTGTTACA CGCATGATAA CTTACCTTTT AAATTAGAAA | 300 |
| AGTCAATAGA TAATTATTAT AGATTGGTGA CATGGAAATA TTTGGACCGA GAAAAAGTCT | 360 |
| CCATCTACAA TATCACAGTG ATAGCCTCAG ATCTAGGAGC CCACTCTGTC ACTGAAACTT | 420 |
| ACATTGCCCT GATTGTGGCA GACACTAATG ACAACCCTCC TCGTTTTCCT CACACCTCCT | 480 |
| ACACAGCCTA TATTCCAGAG AACAACTGA GGGGCGCCTC CATCTTCTCA CTGACTGCAC | 540 |
| ATGATCCTGA CAGTCAGGAA AATGCACAGG TCACTTACTC TGTGTCTGAG GACACCATAC | 600 |
| AGGGAGTGCC TTTGTCTCTT TATATCTCCA TCAACTCAGA TACTGGTGTC CTGTATGCAC | 660 |
| TGCACTCTTT TGACTTCGAG AAGATACAAG ACTTGCAGCT ACTGGTTGTT GCCACTGACA | 720 |
| GTGGAAGCCC ACCTCTCAGC AGCAATGTGT CATTGAGCTT GTTTGTGTTG GACCAGAACG | 780 |
| ACAACGCACC TGAGATTCTA TATCCTAGCT TCCCCACAGA TGGCTCCACT GGTGTGGAAC | 840 |
| TAGCACCCCG CTCTGCAGAG CCTGGATACC TAGTGACCAA AGTGGTGGCA GTGGACAAAG | 900 |
| ACTCAGGACA GAATGCTTGG CTGTCCTACC GTCTGCTGAA GGCCAGCGAA CCTGGGCTCT | 960 |
| TCTCTGTAGG ACTTCACACG GGTGAGGTGC GTACAGCGAG GGCCCTGCTG GACAGAGATG | 1020 |

| | |
|--|------|
| CTCTCAAACA GAATCTGGTG ATGGCCGTGC AGGACCATGG CCAACCCCCT CTCTCGGCCA | 1080 |
| CTGTA ACTCT CACTGTGGCA GTGGCTAACA GCATCCCTGA GGTGTTGGCT GACTTGAGCA | 1140 |
| GCATTAGGAC CCCTGGGGTA CCAGAGGATT CTGATATCAC GCTCCACCTG GTGGTGGCAG | 1200 |
| TGGCTGTGGT CTCCTGTGTC TTCCTTGTCT TTGTCATTGT CCTCCTAGCT CTCAGGCTTC | 1260 |
| AGCGCTGGCA GAAGTCTCGC CAGCTCCAGG GCTCCAAAGG TGGATTGGCT CCTGCACCTC | 1320 |
| CATCACATTT TGTGGGCATC GACGGGGTAC AGGCTTTTCT ACAAACCTAT TCTCATGAAG | 1380 |
| TCTCGCTCAC TTCAGGCTCC CAGACAAGCC ACATTATCTT TCCTCAGCCC AACTATGCAG | 1440 |
| ACATGCTCAT TAACCAAGAA GGCTGTGAGA AAAATGATTC CTTATTAACA TCCATAGATT | 1500 |
| TTCATGAGAG TAACCGTGAA GATGCTTGCG CCCC GCAAGC CCCGCCAAC ACTGACTGGC | 1560 |
| GTTTCTCTCA AGCCCAGAGA CCCGGCACGA GCGGATCCCA AAATGGGGAT GAAACCGGCA | 1620 |
| CCTGGCCCAA CAACCAGTTC GATACAGAGA TGCTGCAAGC CATGATCTTG GCCTCTGCCA | 1680 |
| GTGAAGCCGC TGATGGGAGC TCCACTCTGG GAGGGGGCAC TGGCACTATG GGTTTGAGCG | 1740 |
| CTCGATATGG ACCCCAGTTT ACCCTGCAGC ACGTGCCTGA CTACCGCCAG AACGTGTACA | 1800 |
| TCCCTGGCAG CAATGCCACA CTGACCAACG CAGCTGGCAA ACGAGATGGC AAGGCTCCGG | 1860 |
| CAGGCGGCAA TGGCAACAAC AACAAGTCGG GCAAGAAAGA GAAGAAGTAA TATGGAGGCC | 1920 |
| AGGCCTTGAG CCACAGGGCA GCCTCCCTCC CCAGCCAGTC CAGCTTGTC TTA CTGTAC | 1980 |
| CCAGGCCTCA GAATTTTCAGG GCTCACCCCA GGATTCTGGT AGGAGCCACA GCCAGGCCAT | 2040 |
| GCTCCCCGTT GGGAAACAGA AACAAGTGCC CAAGCCAACA CCCCCTCTTT GTACCCTAGG | 2100 |
| GGGGTTGAAT ATGCAAAGAG AGTTCTGCTG GGACCCCTA TCCAATCAGT GATTGTACCC | 2160 |
| ACATAGGTAG CAGGGTTAGT GTGGATACAC ACACACACAC ACACACACAC ACACACACAA | 2220 |
| CCCTTGTCTT CCGCAGTGCC TGCCACTTTC TGGGACTTTC TCATCCCCCT ACGCCCTTCC | 2280 |
| TTTATCCTCT CCCACCCAGA CACAGCTGCT GGAGAATAAA TTTGGGGATG CTGATGCTAA | 2340 |
| AAAAAAA | 2347 |

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2972 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..1849

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

| | |
|---|-----|
| A GAG GCT GCT CAC CAC CTG GTC CTC ACG GCC TCG GAT GGC GGC AAG | 46 |
| Glu Ala Ala His His Leu Val Leu Thr Ala Ser Asp Gly Gly Lys | |
| 1 5 10 15 | |
| CCG CCT CGC TCT AGC ACA GTG CGC ATC CAC GTG ACA GTG TTG GAT ACA | 94 |
| Pro Pro Arg Ser Ser Thr Val Arg Ile His Val Thr Val Leu Asp Thr | |
| 20 25 30 | |
| AAT GAC AAT GCC CCG GTT TTT CCT CAC CCG ATT TAC CGA GTG AAA GTC | 142 |
| Asn Asp Asn Ala Pro Val Phe Pro His Pro Ile Tyr Arg Val Lys Val | |
| 35 40 45 | |
| CTT GAG AAC ATG CCC CCA GGC ACG CGG CTG CTT ACT GTA ACA GCC AGC | 190 |
| Leu Glu Asn Met Pro Pro Gly Thr Arg Leu Leu Thr Val Thr Ala Ser | |
| 50 55 60 | |
| GAC CCG GAT GAG GGA ATC AAC GGA AAA GTG GCA TAC AAA TTC CGG AAA | 238 |
| Asp Pro Asp Glu Gly Ile Asn Gly Lys Val Ala Tyr Lys Phe Arg Lys | |
| 65 70 75 | |
| ATT AAT GAA AAA CAA ACT CCG TTA TTC CAG CTT AAT GAA AAT ACT GGG | 286 |
| Ile Asn Glu Lys Gln Thr Pro Leu Phe Gln Leu Asn Glu Asn Thr Gly | |
| 80 85 90 95 | |
| GAA ATA TCA ATA GCA AAA AGT CTA GAT TAT GAA GAA TGT TCA TTT TAT | 334 |
| Glu Ile Ser Ile Ala Lys Ser Leu Asp Tyr Glu Glu Cys Ser Phe Tyr | |
| 100 105 110 | |
| GAA ATG GAA ATA CAA GCC GAA GAT GTG GGG GCA CTT CTG GGG AGG ACC | 382 |
| Glu Met Glu Ile Gln Ala Glu Asp Val Gly Ala Leu Leu Gly Arg Thr | |
| 115 120 125 | |
| AAA TTG CTC ATT TCT GTG GAA GAT GTA AAT GAC AAT AGA CCA GAA GTG | 430 |
| Lys Leu Leu Ile Ser Val Glu Asp Val Asn Asp Asn Arg Pro Glu Val | |
| 130 135 140 | |
| ATC ATT ACG TCT TTG TTT AGC CCA GTG TTA GAA AAT TCT CTT CCC GGG | 478 |
| Ile Ile Thr Ser Leu Phe Ser Pro Val Leu Glu Asn Ser Leu Pro Gly | |
| 145 150 155 | |
| ACA GTA ATT GCC TTC TTG AGT GTG CAT GAC CAA GAC TCT GGA AAG AAT | 526 |
| Thr Val Ile Ala Phe Leu Ser Val His Asp Gln Asp Ser Gly Lys Asn | |
| 160 165 170 175 | |
| GGT CAA GTT GTC TGT TAC ACA CGT GAT AAT TTA CCT TTT AAA TTA GAA | 574 |
| Gly Gln Val Val Cys Tyr Thr Arg Asp Asn Leu Pro Phe Lys Leu Glu | |
| 180 185 190 | |
| AAG TCA ATA GGT AAT TAT TAT AGA TTA GTG ACA AGG AAA TAT TTG GAC | 622 |
| Lys Ser Ile Gly Asn Tyr Tyr Arg Leu Val Thr Arg Lys Tyr Leu Asp | |
| 195 200 205 | |
| CGA GAA AAT GTC TCT ATC TAC AAT ATC ACA GTG ATG GCC TCA GAT CTA | 670 |
| Arg Glu Asn Val Ser Ile Tyr Asn Ile Thr Val Met Ala Ser Asp Leu | |
| 210 215 220 | |
| GGA ACA CCA CCT CTG TCC ACT GAA ACT CAA ATC GCT CTG CAC GTG GCA | 718 |
| Gly Thr Pro Pro Leu Ser Thr Glu Thr Gln Ile Ala Leu His Val Ala | |
| 225 230 235 | |

| | | | | | | | | | | | | | | | | |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| GAC Asp 240 | ATT Ile | AAC Asn | GAC Asp | AAC Asn | CCT Pro | CCT Pro | ACT Thr | TTC Phe | CCT Pro | CAT His | GCC Ala | TCC Ser | TAC Tyr | TCA Ser | GCG Ala 255 | 766 |
| TAT Tyr | ATC Ile | CTA Leu | GAG Glu | AAC Asn 260 | AAC Asn | CTG Leu | AGA Arg | GGA Gly | GCC Ala 265 | TCC Ser | ATC Ile | TTT Phe | TCC Ser | TTG Leu 270 | ACT Thr | 814 |
| GCA Ala | CAC His | GAC Asp | CCC Pro 275 | GAC Asp | AGC Ser | CAG Gln | GAG Glu | AAT Asn 280 | GCC Ala | CAG Gln | GTC Val | ACT Thr | TAC Tyr | TCT Ser | GTG Val | 862 |
| ACC Thr | GAG Glu | GAC Asp 290 | ACG Thr | CTG Leu | CAG Gln | GGG Gly | GCG Ala 295 | CCC Pro | CTG Leu | TCC Ser | TCG Ser | TAT Tyr 300 | ATC Ile | TCC Ser | ATC Ile | 910 |
| AAC Asn 305 | TCT Ser | GAC Asp | ACC Thr | GGT Gly | GTC Val | CTG Leu 310 | TAT Tyr | GCG Ala | CTG Leu | CAA Gln | TCT Ser 315 | TTT Phe | GAC Asp | TAT Tyr | GAG Glu | 958 |
| CAG Gln 320 | ATC Ile | CGA Arg | GAC Asp | CTG Leu | CAG Gln 325 | CTA Leu | CTG Leu | GTA Val | ACA Thr | GCC Ala 330 | AGC Ser | GAC Asp | AGC Ser | GGG Gly | GAC Asp 335 | 1006 |
| CCG Pro | CCC Pro | CTC Leu | AGC Ser | AGC Ser 340 | AAC Asn | ATG Met | TCA Ser | CTG Leu | AGC Ser 345 | CTG Leu | TTC Phe | GTG Val | CTG Leu | GAC Asp 350 | CAG Gln | 1054 |
| AAT Asn | GAC Asp | AAC Asn 355 | GCG Ala | CCC Pro | GAG Glu | ATC Ile | CTG Leu | TAC Tyr 360 | CCC Pro | GCC Ala | CTC Leu | CCC Pro | ACA Thr 365 | GAC Asp | GGT Gly | 1102 |
| TCC Ser | ACT Thr | GGC Gly 370 | GTG Val | GAG Glu | CTG Leu | GCG Ala | CCC Pro 375 | CGC Arg | TCC Ser | GCA Ala | GAG Glu | CGT Arg 380 | GGC Gly | TAC Tyr | CTG Leu | 1150 |
| GTG Val | ACC Thr 385 | AAG Lys | GTG Val | GTG Val | GCG Ala | GTG Val 390 | GAC Asp | AGA Arg | GAC Asp | TCG Ser | GGC Gly 395 | CAG Gln | AAC Asn | GCC Ala | TGG Trp | 1198 |
| CTG Leu 400 | TCC Ser | TAC Tyr | CGC Arg | CTG Leu | CTC Leu 405 | AAG Lys | GCC Ala | AGC Ser | GAG Glu | CCG Pro 410 | GGA Gly | CTC Leu | TTC Phe | TCG Ser | GTG Val 415 | 1246 |
| GGT Gly | CTG Leu | CAC His | ACG Thr | GGC Gly 420 | GAG Glu | GTG Val | CGC Arg | ACG Thr | GCG Ala 425 | CGA Arg | GCC Ala | CTG Leu | CTG Leu | GAC Asp 430 | AGA Arg | 1294 |
| GAC Asp | GCG Ala | CTC Leu | AAG Lys 435 | CAG Gln | AGC Ser | CTC Leu | GTG Val | GTG Val 440 | GCC Ala | GTC Val | CAG Gln | GAC Asp | CAT His 445 | GGC Gly | CAG Gln | 1342 |
| CCC Pro | CCT Pro | CTC Leu 450 | TCC Ser | GCC Ala | ACT Thr | GTC Val | ACG Thr 455 | CTC Leu | ACC Thr | GTA Val | GCC Ala | GTG Val 460 | GCT Ala | GAC Asp | AGC Ser | 1390 |
| ATC Ile 465 | CCC Pro | GAA Glu | GTC Val | CTG Leu | ACC Thr | GAG Glu 470 | TTG Leu | GGC Gly | AGT Ser | CTG Leu | AAG Lys 475 | CCT Pro | TCG Ser | GTC Val | GAC Asp | 1438 |

| | |
|---|------|
| CCG AAC GAT TCG AGC CTT ACA CTC TAT CTC GTG GTG GCA GTG GCT GCC | 1486 |
| Pro Asn Asp Ser Ser Leu Thr Leu Tyr Leu Val Val Ala Val Ala Ala | |
| 480 485 490 495 | |
| ATC TCC TGT GTC TTC CTC GCC TTT GTC GCT GTG CTT CTG GGG CTC AGG | 1534 |
| Ile Ser Cys Val Phe Leu Ala Phe Val Ala Val Leu Leu Gly Leu Arg | |
| 500 505 510 | |
| CTG AGG CGC TGG CAC AAG TCA CGC CTG CTC CAG GAT TCC GGT GGC AGA | 1582 |
| Leu Arg Arg Trp His Lys Ser Arg Leu Leu Gln Asp Ser Gly Gly Arg | |
| 515 520 525 | |
| TTG GTA GGC GTG CCT GCC TCA CAT TTT GTG GGT GTT GAG GAG GTA CAG | 1630 |
| Leu Val Gly Val Pro Ala Ser His Phe Val Gly Val Glu Val Gln | |
| 530 535 540 | |
| GCT TTC CTG CAG ACC TAT TCC CAG GAA GTC TCC CTC ACC GCC GAC TCG | 1678 |
| Ala Phe Leu Gln Thr Tyr Ser Gln Glu Val Ser Leu Thr Ala Asp Ser | |
| 545 550 555 | |
| CGG AAG AGT CAC CTG ATC TTT CCC CAG CCC AAC TAC GCA GAC ATG CTC | 1726 |
| Arg Lys Ser His Leu Ile Phe Pro Gln Pro Asn Tyr Ala Asp Met Leu | |
| 560 565 570 575 | |
| ATC AGT CAG GAG GGC TGT GAG AAA AAT GAT TCT TTG TTA ACA TCC GTA | 1774 |
| Ile Ser Gln Glu Gly Cys Glu Lys Asn Asp Ser Leu Leu Thr Ser Val | |
| 580 585 590 | |
| GAT TTT CAT GAA TAT AAG AAT GAA GCT GAT CAT GGT CAG GTG AGT TTA | 1822 |
| Asp Phe His Glu Tyr Lys Asn Glu Ala Asp His Gly Gln Val Ser Leu | |
| 595 600 605 | |
| GTT CTT TGC TTG CTT TTA ATT TCC AGA TGAATTTTAT TTGGCATAAA | 1869 |
| Val Leu Cys Leu Leu Leu Ile Ser Arg | |
| 610 615 | |
| TTATGTTTTG AAAACATTG TGAAGATAGT TGAAAATAAT TTTTAAGGTG TATCACAGAG | 1929 |
| TTTTGGGTTT ATTTTGGTGG TGTTACCAAA AAATTGAACT CTAATAGTCA TAGGTTATTG | 1989 |
| TTTCATTTGC TTTTAAACGA CTTGGAAAAG ATTGTTCCAC CATTTTAAAC CTTCCAGTAT | 2049 |
| TTTATTCCTA TTATCACTCA TTCACTTAAG AAGTAGCTAC CCGTCCATAC TGGTAATTTT | 2109 |
| GCTATTGTTT GTTTGTGTGT GTGTGTGTGT GTGTGTGTGT GTGTGTGTAT CCCAACTAG | 2169 |
| AACTTCAGAA AATTATCAAG AAGTCTAAAG CCTTGTTATT AGCTTAGCAA AAGTAAAATA | 2229 |
| TATCTCAGAA TTTTATAGGT TATGTTTAGC ATTTGAACCT GTAAGTAGGC TCTTGATAT | 2289 |
| TTCTTCACTT TAAACCTCTT TTCTGAGCCC TGTTTCTGTA CCAGTGCCCT TCAAACTTT | 2349 |
| AATACTTCTT ACCATCCTTC AAAACATGAA CAAACTTTAA AGATGGATCT TGGTGGGAGA | 2409 |
| TGAGACTGGT TACTAAATAT TAAGTATGTG AGTCAGTGGT CACCTGGGCT CCATCCCCAT | 2469 |
| GGAGACATGA AATCTAAAGC CTAGAATGTC CATTGCTCCC CCAAACAAA AACAAAAGCA | 2529 |
| AAAACATTAG ATCTGAATTA AAATGTAATT TTAACTGTT GAAAGTGAAT TTTGTAAAT | 2589 |
| ATGTAAGAAC ATATTTCAAT ACAATTCCAA TTAGCTGTTT CGGTTGTGCA TTGATGTGAA | 2649 |

| | |
|--|------|
| GTGGTGAGAA TGTTGATATT AAGAACCAAT GTTTCAGGTA CACAAGTTCT AAATAAGCTG | 2709 |
| ATCAATTCAA TTAAAGTTAT TCAGTCTTGG CTGGACACAG TGCCTCATGT CTGAAATCCC | 2769 |
| AGCACTTTGG GAGGCTGGGG CAGGAGGACC GCTTGAGCCC CGGGGGTTTG AAACCTGCAGT | 2829 |
| GAGCTATGAT CATGCCACTG CACTCCAGCC TAGGTGGCAG AACTAGACCC TGTCTCTAAA | 2889 |
| AAACTATTA TTAGGCCGCG TCGGGTGGCT CACGCCTGTA ATCCCAGCAC TTTGGGAGAC | 2949 |
| TGAGGTGGGT GGATCACCTG AGC | 2972 |

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 616 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Ala | Ala | His | His | Leu | Val | Leu | Thr | Ala | Ser | Asp | Gly | Gly | Lys | Pro | 1 | 5 | 10 | 15 |
| Pro | Arg | Ser | Ser | Thr | Val | Arg | Ile | His | Val | Thr | Val | Leu | Asp | Thr | Asn | 20 | 25 | 30 | |
| Asp | Asn | Ala | Pro | Val | Phe | Pro | His | Pro | Ile | Tyr | Arg | Val | Lys | Val | Leu | 35 | 40 | 45 | |
| Glu | Asn | Met | Pro | Pro | Gly | Thr | Arg | Leu | Leu | Thr | Val | Thr | Ala | Ser | Asp | 50 | 55 | 60 | |
| Pro | Asp | Glu | Gly | Ile | Asn | Gly | Lys | Val | Ala | Tyr | Lys | Phe | Arg | Lys | Ile | 65 | 70 | 75 | 80 |
| Asn | Glu | Lys | Gln | Thr | Pro | Leu | Phe | Gln | Leu | Asn | Glu | Asn | Thr | Gly | Glu | 85 | 90 | 95 | |
| Ile | Ser | Ile | Ala | Lys | Ser | Leu | Asp | Tyr | Glu | Glu | Cys | Ser | Phe | Tyr | Glu | 100 | 105 | 110 | |
| Met | Glu | Ile | Gln | Ala | Glu | Asp | Val | Gly | Ala | Leu | Leu | Gly | Arg | Thr | Lys | 115 | 120 | 125 | |
| Leu | Leu | Ile | Ser | Val | Glu | Asp | Val | Asn | Asp | Asn | Arg | Pro | Glu | Val | Ile | 130 | 135 | 140 | |
| Ile | Thr | Ser | Leu | Phe | Ser | Pro | Val | Leu | Glu | Asn | Ser | Leu | Pro | Gly | Thr | 145 | 150 | 155 | 160 |
| Val | Ile | Ala | Phe | Leu | Ser | Val | His | Asp | Gln | Asp | Ser | Gly | Lys | Asn | Gly | 165 | 170 | 175 | |
| Gln | Val | Val | Cys | Tyr | Thr | Arg | Asp | Asn | Leu | Pro | Phe | Lys | Leu | Glu | Lys | 180 | 185 | 190 | |

Ser Ile Gly Asn Tyr Tyr Arg Leu Val Thr Arg Lys Tyr Leu Asp Arg
195 200 205

Glu Asn Val Ser Ile Tyr Asn Ile Thr Val Met Ala Ser Asp Leu Gly
210 215 220

Thr Pro Pro Leu Ser Thr Glu Thr Gln Ile Ala Leu His Val Ala Asp
225 230 235 240

Ile Asn Asp Asn Pro Pro Thr Phe Pro His Ala Ser Tyr Ser Ala Tyr
245 250 255

Ile Leu Glu Asn Asn Leu Arg Gly Ala Ser Ile Phe Ser Leu Thr Ala
260 265 270

His Asp Pro Asp Ser Gln Glu Asn Ala Gln Val Thr Tyr Ser Val Thr
275 280 285

Glu Asp Thr Leu Gln Gly Ala Pro Leu Ser Ser Tyr Ile Ser Ile Asn
290 295 300

Ser Asp Thr Gly Val Leu Tyr Ala Leu Gln Ser Phe Asp Tyr Glu Gln
305 310 315 320

Ile Arg Asp Leu Gln Leu Leu Val Thr Ala Ser Asp Ser Gly Asp Pro
325 330 335

Pro Leu Ser Ser Asn Met Ser Leu Ser Leu Phe Val Leu Asp Gln Asn
340 345 350

Asp Asn Ala Pro Glu Ile Leu Tyr Pro Ala Leu Pro Thr Asp Gly Ser
355 360 365

Thr Gly Val Glu Leu Ala Pro Arg Ser Ala Glu Arg Gly Tyr Leu Val
370 375 380

Thr Lys Val Val Ala Val Asp Arg Asp Ser Gly Gln Asn Ala Trp Leu
385 390 395 400

Ser Tyr Arg Leu Leu Lys Ala Ser Glu Pro Gly Leu Phe Ser Val Gly
405 410 415

Leu His Thr Gly Glu Val Arg Thr Ala Arg Ala Leu Leu Asp Arg Asp
420 425 430

Ala Leu Lys Gln Ser Leu Val Val Ala Val Gln Asp His Gly Gln Pro
435 440 445

Pro Leu Ser Ala Thr Val Thr Leu Thr Val Ala Val Ala Asp Ser Ile
450 455 460

Pro Glu Val Leu Thr Glu Leu Gly Ser Leu Lys Pro Ser Val Asp Pro
465 470 475 480

Asn Asp Ser Ser Leu Thr Leu Tyr Leu Val Val Ala Val Ala Ala Ile
485 490 495

Ser Cys Val Phe Leu Ala Phe Val Ala Val Leu Leu Gly Leu Arg Leu
500 505 510

Arg Arg Trp His Lys Ser Arg Leu Leu Gln Asp Ser Gly Gly Arg Leu
515 520 525

Val Gly Val Pro Ala Ser His Phe Val Gly Val Glu Glu Val Gln Ala
530 535 540

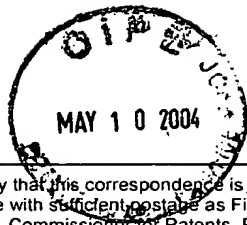
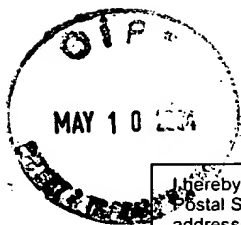
Phe Leu Gln Thr Tyr Ser Gln Glu Val Ser Leu Thr Ala Asp Ser Arg
545 550 555 560

Lys Ser His Leu Ile Phe Pro Gln Pro Asn Tyr Ala Asp Met Leu Ile
565 570 575

Ser Gln Glu Gly Cys Glu Lys Asn Asp Ser Leu Leu Thr Ser Val Asp
580 585 590

Phe His Glu Tyr Lys Asn Glu Ala Asp His Gly Gln Val Ser Leu Val
595 600 605

Leu Cys Leu Leu Leu Ile Ser Arg
610 615



I hereby certify that this correspondence is being deposited with the U.S. Postal Service with sufficient postage as First Class Mail, in an envelope addressed to: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450, on the date shown below.

Dated: 5-7-04

Signature: Katherine L. Neville

Katherine L. Neville, Ph.D.

Docket No.: 27866/37501
(PATENT)

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re , Application of: Suzuki, S.

Application No.: 09/880,573

Group Art Unit: 1647

Filed: June 13, 2001

Examiner: David Romeo

For: Protocadherin Materials and Methods

STATEMENT UNDER 37 C.F.R. §1.821

Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Dear Sir:

I hereby state that the content of the paper and computer readable copies of the Sequence Listing, submitted herewith in accordance with 37 C.F.R. §§1.821 and 1.825, are the same and include no new matter.

May 7, 2004

Respectfully submitted,

MARSHALL, GERSTEIN & BORUN LLP
6300 Sears Tower
233 South Wacker Drive
Chicago, Illinois 60606-6357
(312) 474-6300

By: Katherine L. Neville

Katherine L. Neville, Ph.D.

Reg. No. 53,379

Agent for Applicants



| | | | | |
|-------|------|-------|--|-------|
| PC43 | EC 1 | (29) | ASTVIHVEIPEEREK-----GFAVGNVUANL--GLDLGSLSA-- | (63) |
| | EC 2 | (136) | PTQEMKLEISEAVAP-----GTRFPLESAH---DPDLGSNSL-- | (169) |
| | EC 3 | (245) | NQSLYRARVPGGCTS-----GTRVQVQLAT---DLDEGPNGE-- | (278) |
| | EC 4 | (353) | TVTSVYSPVPEDAS-----GTVIALLSVT---DLDAGENGL-- | (385) |
| | EC 5 | (457) | SOSSYDVYIEENNLP-----GAPILNLSVW---DPDAPQONAR-- | (490) |
| | EC 6 | (567) | LYPRPGSSVEMLPRTSA-GHLVSRVVGW----DADAGHNAW-- | (604) |
| PC42 | EC 1 | (42) | VPEEQPNTLI-----GSL-----AADYGFPDVG-- | (65) |
| | EC 2 | (147) | ASPVITTLAIPENTNI-----GSLFPIPLAS---DRDAGPNGV-- | (180) |
| | EC 3 | (247) | ERPSYEAELSENSPI-----GHSVIOVKAN---DSDQGANAEE-- | (280) |
| | EC 4 | (354) | EIRGIGLVTHODGMANISEDVAETAVALVQVSDRDEGENAA-- | (395) |
| | EC 5 | (473) | TQSVTEVAFFPENNKP-----GEVIAEITAS---DADSGSNAE-- | (506) |
| | EC 6 | (579) | MLSGYNFVSMENMPA-----LSPVGMVTVI---DGDKGENAQ-- | (612) |
| | EC 7 | (682) | TAPSNNTSHKLLTPQTRL---GETVSQVAEE---DFDSGVNAE-- | (717) |
| FAT | EC18 | (1) | EDTVYSFDIPENAOAOR-----GYQVGQIVAR---DADLGQNAQ-- | (34) |
| N-CAD | EC 1 | (1) | DWVIPPINLPENSRG-----PFPQELVRIRS---DRDKNLSLRYT | (37) |
| | EC 2 | (109) | LHQVWNGSVPEGSKP-----GTVYMTVTAI---DADDPNALNGM | (144) |
| | EC 3 | (224) | TAMTFYGEVPENRVD-----IIVANLTVT---DKDQPHTPAWN | (258) |
| | EC 4 | (339) | APNPKIIRQEEGLHA-----GTMLTTFTAG---DPDRYMQQN-- | (372) |
| | EC 5 | (447) | LPQEAETCETDPNSINITAL-----DYDIDPNAGP-- | (478) |

****0***v*EN***-----GT*v**v*A*-----D*D*G*N*-----

MOTIF

FIGURE 1A



| | | | | |
|-------|------|-------|---|-------|
| PC43 | EC 1 | (64) | RRFPVVGASRR-----FFEVRNRET-----GEMFVNDR----- | (91) |
| | EC 2 | (170) | QTYELSRNEY-----FALRVQTRDSTKYAELVLERA-- | (201) |
| | EC 3 | (279) | IIYSFGSHNRAGVRQL--FALDLVT-----GMLTIKGR---- | (309) |
| | EC 4 | (386) | VTCEVPPGLP-----FSLTSSLKNYFTLKTSAD----- | (413) |
| | EC 5 | (491) | LSFFLLEQGAETGLVGRYFTINRDN-----GIVSSLVP---- | (523) |
| | EC 6 | (605) | LSYSLFGSPNOSL-----FAIGLHT-----GQISTARPV--- | (633) |
| PC42 | EC 1 | (66) | HLYKLEVGAPE-----YLRVDGKT-----GDIFTTETS--- | (92) |
| | EC 2 | (181) | ASYELQVAED-----QEEKQPQLIVMGN----- | (203) |
| | EC 3 | (281) | IEYTFHOAPEVVRRL---LRLDRNT-----GLITVQGP----- | (310) |
| | EC 4 | (396) | VTCVVAGDVP-----FOLROASETGSDSKKYFLOTTTP | (429) |
| | EC 5 | (507) | LVYSLEPEPAKGL-----FTISPET-----GEIQVKT----- | (535) |
| | EC 6 | (613) | VQLSVEODNGD-----FVIONGT-----GTILSSLS----- | (638) |
| | EC 7 | (718) | LIYSIAGGNPYGL-----FOIGSHS-----GAITLEKE----- | (745) |
| FAT | EC18 | (35) | LSYGVVSDWANDV-----FSLNPQT-----GMLTLTAR---- | (62) |
| N-CAD | EC 1 | (38) | VTGPGADQPPTGI-----FIINPIS-----GQLSVTKP----- | (65) |
| | EC 2 | (145) | LRYRILSOAPSTSPNM-FINNNET-----GDIITVAAG---- | (177) |
| | EC 3 | (259) | AVTRISGGDPTGR-----FAIQTDPNND-GLVTVVKP----- | (290) |
| | EC 4 | (373) | IRYTKLSDPAN-----WLKIDPVN-----GOITTIIV----- | (399) |
| | EC 5 | (479) | FAYDLPLSPVTIKRN---WTITRLN-----GDFAQLNLK---- | (509) |

MOTIF I*O*I*****O*I***T-----G*I*T***-----

FIGURE 1B

| | | | | |
|-------|------|-------|--|-------|
| PC43 | EC 1 | (92) | LDREELCGTLPCTVTLVLVNP-----LELFSVEVVIODINDNNPAF | (135) |
| | EC 2 | (202) | LDREEPSLQLVLTALDGGTPAL-----SASLPHIKVLANDNAPVF | (244) |
| | EC 3 | (310) | LDGEDTKLHEIYIOAKDGANPE-----GAHCKVLVEVDVNDNAPEI | (352) |
| | EC 4 | (414) | LDRETVPEYNLSITARDAGTSL-----SALTIVRVQVSDINDNPPQS | (456) |
| | EC 5 | (524) | LDYEDRRREFELTAHISDGGTPVL-----ATNISVNI FVTD RNDNAPQV | (566) |
| | EC 6 | (634) | ODTDSPRQTLTVL-IKDNGEPSLTTATLTVSVTEDSPEARAEFPGSAPREQKN | (688) |
| PC42 | EC 1 | (93) | IDREGLRECONQLPGDPCILEFEVSITDLVQNAS--PRLLEGOIEVODINDNTPNF | (146) |
| | EC 2 | (204) | LDRERWDSYDLTIKVODGGSPPR-----ATSALLRVTVLDTNDNAPKF | (246) |
| | EC 3 | (311) | VDREDLSTLRFSLAKDRGTNPK-----SARQVVTVTKMDNDNAPTI | (353) |
| | EC 4 | (430) | LDYEKVKDYTIEIVAVDSGNPPL-----SSTNSLKQVVVDVNDNAPVF | (472) |
| | EC 5 | (536) | LDREQRESYELKVVAADRGSPL-----QGTATVLNVVLDNCNDNDPKF | (578) |
| | EC 6 | (639) | FDREQQSTYTFQLKAVDGGVPPR-----SAYVGTINVL DENDNAPYI | (681) |
| | EC 7 | (746) | IERRHGLHRLVVKVSDRGKPPRYGTALVHLYVNETLANRTLLETLLGHSLDTPLD | (801) |
| | | | (802) IDIAGDPEYERSKQRGN | (818) |
| FAT | EC18 | (63) | LDYEEVQHYIILIVOAODNGQPSL-----STTITVYCNVLDLNDNAPIF | (105) |
| N-CAD | EC 1 | (66) | LDREQIARFHLRAHAVDINGNQV-----ENPIDIVINVIDMNDNRPEF | (108) |
| | EC 2 | (178) | LDREKVQQYTLIIQATDMEGNPTYGL-----SNTATAVITTVTDVNDNPPEF | (223) |
| | EC 3 | (291) | IDFETNRMFVLTVAAENQVPLAKGIOHPP-----QSTATSVTVTDVNE-NPYF | (338) |
| | EC 4 | (400) | LDRESPNVKNNIYNATFLASDNGIIPPM-----SGTGLQIYLLDINDNAPQV | (446) |
| | EC 5 | (510) | IKFLEAGIYEVPIIITDSGNPPKSNKS-----ILRVRCQCFNGDCTDVDR | (557) |
| MOTIF | | | LDRE****O*L*v*A*D*G*P**-----**T*TV*v*v*D*NDNAP*F | |

FIGURE 1C